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OM protein - protein search, using sw model

Run on: November 19, 2004, 20:57:38 ; Search time 61.2534 Seconds
(without alignments)
1019.028 Million cell updates/sec

Title: US-10-014-363-3

Perfect score: 894

Sequence: 1 APPRIEGRAPRLICDSRVL.....NFLRLKGLKLTGEACRTGDR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	894	100.0	174	5	Abb77898 Amino aci
2	894	100.0	201	5	Abb77901 Amino aci
3	861	96.3	174	5	Abb77900 Amino aci
4	861	96.3	201	5	Abb77903 Amino aci
5	859	96.1	412	2	AAW33354 Oligopept
6	856.5	95.8	169	5	Abb77899 Amino aci
7	856.5	95.8	196	5	Abb77902 Amino aci
8	856	95.7	167	1	AAp50298 Human rec
9	855	95.6	425	7	Abu64199 Plasmid p
10	855	95.6	425	8	Ado10511 Kb signal
11	854	95.5	205	8	Adj71846 Non-glyco
12	851	95.2	166	1	AAp70398 Sequence
13	851	95.2	166	2	AAr23593 Recombina
14	851	95.2	166	2	AAW58404 Human ery
15	851	95.2	166	2	AAW7780 Human EPO
16	851	95.2	166	3	ABB07030 Modified
17	851	95.2	166	4	ABB83622 Protein #
18	851	95.2	166	4	AAE02641 Human ery
19	851	95.2	166	4	AAb66698 Human ery
20	851	95.2	166	5	ABG92101 Human ery
21	851	95.2	166	5	AAW53062 Human ery
22	851	95.2	166	5	ABB77897 Amino aci
23	851	95.2	166	5	ADG65661 Human ery
24	851	95.2	166	6	ABr39996 Human ery
25	851	95.2	166	6	ABr57500 Human ery

26	851	95.2	166	7	ADf70839 Human ery
27	851	95.2	166	8	ADL92150 Erythrope
28	851	95.2	166	8	ADK70564 Human ery
29	851	95.2	166	8	ADL88867 Human cyt
30	851	95.2	166	8	ADL06781 Human 166
31	851	95.2	166	8	ADo59416 Human 166
32	851	95.2	167	1	AAp50299 Human rec
33	851	95.2	188	1	AAp60599 Clone lam
34	851	95.2	188	1	AAp81195 Erythrope
35	851	95.2	193	1	AAp50300 Human ery
36	851	95.2	193	1	AAp60597 Clone lam
37	851	95.2	193	1	AAp70256 Sequence
38	851	95.2	193	2	AAp65499 Human pre
39	851	95.2	193	2	AAr71137 Human ery
40	851	95.2	193	2	AAr74141 Human ery
41	851	95.2	193	2	AAr81982 Human ery
42	851	95.2	193	2	AAr98397 Human ery
43	851	95.2	193	3	AAy43398 Human ery
44	851	95.2	193	3	AAy94530 Human ery
45	851	95.2	193	3	AAy93638 Amino aci

ALIGNMENTS

RESULT 1
ABB77898
ID ABB77898 standard; protein; 174 AA.
XX ABB77898;
XX AC
XX
DT 07-OCT-2002 (first entry)
XX
DE Amino acid sequence of a modified human erythropoietin (EPO).
XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
KW red blood cell production; anaemia; chronic renal failure;
KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
KW committed erythroid progenitor.
XX Synthetic.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Cleavage-site 1..8
FT /note= "proteolytic cleavage site"
FT Protein 9..174
FT /note= "EPO protein"
XX
XX WO200249673-A2.
XX 27-JUN-2002.
XX 08-DEC-2001; 2001WO-EP014434.
XX 20-DEC-2000; 2000EP-00127891.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
XX Wozny M;
XX WPI; 2002-566640/60.
XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
PT useful for treating diseases correlated with anemia in chronic renal
PT failure patients and acquired immunodeficiency syndrome.
XX Disclosure; Page 38-39; 40pp; English.
PS The present sequence represents a modified human erythropoietin (EPO)
CC protein. The EPO was extended at the N-terminal by a proteolytic cleavage
CC site. It was used to produce conjugates of the invention. The

CC specification describes a conjugate comprising an EPO glycoprotein having
 CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 CC or a rearrangement of a glycosylation site). The glycoprotein is
 CC covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 CC has in vivo biological activity of causing bone marrow cells to increase
 CC production of reticulocytes and red blood cells. The conjugate increased
 CC circulating half-life and plasma residence time, decreased clearance,
 CC increased clinical activity in vivo, improved potency and stability, when
 CC compared to unmodified EPO. The EPO conjugate is useful for preparing
 CC medicaments for the treatment and prophylaxis of diseases correlated with
 CC anaemia in chronic renal failure patients (CRF), acquired
 CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow
 XX
 SQ Sequence 174 AA;

Query Match 100.0%; Score 894; DB 5; Length 174;
 Best Local Similarity 100.0%; Pred. No. 3.1e-91;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APPRIEGRAPPLICDSRVLLERLLEAKEAENITTCGAHCNLENITVPTDKVNFYAWK 60
 DB 1 APPRIEGRAPPLICDSRVLLERLLEAKEAENITTCGAHCNLENITVPTDKVNFYAWK 60
 QY 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLRSLTTLRAL 120
 DB 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLRSLTTLRAL 120
 QY 121 GAOKEAISPPDAASAAPLRTITADTFKLPFRVSNFLRGKLYTGACRTGDR 174
 DB 121 GAOKEAISPPDAASAAPLRTITADTFKLPFRVSNFLRGKLYTGACRTGDR 174

RESULT 2

ABB77901
 ID ABB77901 standard; protein; 201 AA.

AC ABB77901;

DT 07-OCT-2002 (first entry)

DE Amino acid sequence of a modified human erythropoietin (EPO).

XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..27

FT /note= "secretion signal peptide"

FT Cleavage-site 28..35

FT /note= "proteolytic cleavage site"

FT Protein 36..201

FT /note= "EPO protein"

XX W0200249673-A2.

XX 27-JUN-2002.

XX 08-DEC-2001; 2001WO-EP014434.

XX 20-DEC-2000; 2000EP-00127891.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;

PI Wozny M;
 XX
 DR WPI; 2002-566640/60.
 DR N-PSDB; ABL59289.
 XX
 PT Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 PT useful for treating diseases correlated with anemia in chronic renal
 PT failure patients and acquired immunodeficiency syndrome.
 XX
 XX Disclosure; Fig 3; 40pp; English.

XX The present sequence represents a modified human erythropoietin (EPO)
 CC protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 CC site. It was used to produce conjugates of the invention. The
 CC specification describes a conjugate comprising an EPO glycoprotein having
 CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 CC or a rearrangement of a glycosylation site). The glycoprotein is
 CC covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 CC has in vivo biological activity of causing bone marrow cells to increase
 CC production of reticulocytes and red blood cells. The conjugate increased
 CC circulating half-life and plasma residence time, decreased clearance, when
 CC compared to unmodified EPO. The EPO conjugate is useful for preparing
 CC medicaments for the treatment and prophylaxis of diseases correlated with
 CC anaemia in chronic renal failure patients (CRF), acquired
 CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow
 XX

SQ Sequence 201 AA;

Query Match 100.0%; Score 894; DB 5; Length 201;
 Best Local Similarity 100.0%; Pred. No. 3.1e-91;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRIEGRAPPLICDSRVLLERLLEAKEAENITTCGAHCNLENITVPTDKVNFYAWK 60

DB 28 APPRIEGRAPPLICDSRVLLERLLEAKEAENITTCGAHCNLENITVPTDKVNFYAWK 87

QY 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLRSLTTLRAL 120

DB 88 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLRSLTTLRAL 147

QY 121 GAOKEAISPPDAASAAPLRTITADTFKLPFRVSNFLRGKLYTGACRTGDR 174

DB 148 GAOKEAISPPDAASAAPLRTITADTFKLPFRVSNFLRGKLYTGACRTGDR 201

RESULT 3

ABB77900

ID ABB77900 standard; protein; 174 AA.

AC ABB77900;

DT 07-OCT-2002 (first entry)

DE Amino acid sequence of a modified human erythropoietin (EPO).

XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Cleavage-site 1..8

FT /note= "proteolytic cleavage site"

FT Protein 9..174

FT /note= "EPO protein"

XX WO200249673-A2.
 XX 27-JUN-2002.
 XX 08-DEC-2001; 2001WO-EP014434.
 XX 20-DEC-2000; 2000EP-00127891.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 XX Wozny M;
 XX WPI; 2002-566640/60.
 XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 XX useful for treating diseases correlated with anemia in chronic renal
 XX failure patients and acquired immunodeficiency syndrome.
 XX Disclosure; Page 39-40; 40pp; English.
 XX The present sequence represents a modified human erythropoietin (EPO)
 XX protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 XX site. It was used to produce conjugates of the invention. The
 XX specification describes a conjugate comprising an EPO glycoprotein having
 XX an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 XX analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 XX or a rearrangement of a glycosylation site). The glycoprotein is
 XX covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 XX has in vivo biological activity of causing bone marrow cells to increase
 XX production of reticulocytes and red blood cells. The conjugate increased
 XX circulating half-life and plasma residence time, decreased clearance,
 XX increased clinical activity in vivo, improved potency and stability, when
 XX compared to unmodified EPO. The EPO conjugate is useful for preparing
 XX medicaments for the treatment and prophylaxis of diseases correlated with
 XX anaemia in chronic renal failure patients (CRF), acquired
 XX immunodeficiency syndrome (AIDS) and for treating cancer patients
 XX undergoing chemotherapy. It is also useful for treating patients by
 XX stimulating the division and differentiation of committed erythroid
 XX progenitors in the bone marrow
 XX Sequence 174 AA;

Query Match 96.3%; Score 861; DB 5; Length 174;
 Best Local Similarity 97.1%; Pred. No. 1.5e-87;
 Matches 169; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 APPRIEGRAPPRILICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPTKVNFAWK 60
 DB 1 APFGAAHYAPPRILICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPTKVNFAWK 60
 QY 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLRAL 120
 DB 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLRAL 120
 QY 121 GAOKEAISPPDAASAAPLRTITADTFKLFVSVNFRGLKLYTGACRTGDR 174
 DB 121 GAOKEAISPPDAASAAPLRTITADTFKLFVSVNFRGLKLYTGACRTGDR 174

RESULT 4
 ABB77903
 ID ABB77903 standard; protein; 201 AA.
 AC ABB77903;
 XX 07-OCT-2002 (first entry)
 XX Amino acid sequence of a modified human erythropoietin (EPO).
 XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 XX red blood cell production; anaemia; chronic renal failure;

KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.
 OS Synthetic.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..27
 FT /note= "secretion signal peptide"
 FT Cleavage-site 28..35
 FT /note= "proteolytic cleavage site"
 FT Protein 36..201
 FT /note= "EPO protein"
 XX WO200249673-A2.
 XX 27-JUN-2002.
 XX 08-DEC-2001; 2001WO-EP014434.
 XX 20-DEC-2000; 2000EP-00127891.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 XX Wozny M;
 XX WPI; 2002-566640/60.
 XX N-PSDB; ABL59291.
 XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 XX useful for treating diseases correlated with anemia in chronic renal
 XX failure patients and acquired immunodeficiency syndrome.
 XX Disclosure; Fig 5; 40pp; English.
 XX The present sequence represents a modified human erythropoietin (EPO)
 XX protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 XX site. It was used to produce conjugates of the invention. The
 XX specification describes a conjugate comprising an EPO glycoprotein having
 XX an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 XX analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 XX or a rearrangement of a glycosylation site). The glycoprotein is
 XX covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 XX has in vivo biological activity of causing bone marrow cells to increase
 XX production of reticulocytes and red blood cells. The conjugate increased
 XX circulating half-life and plasma residence time, decreased clearance,
 XX increased clinical activity in vivo, improved potency and stability, when
 XX compared to unmodified EPO. The EPO conjugate is useful for preparing
 XX medicaments for the treatment and prophylaxis of diseases correlated with
 XX anaemia in chronic renal failure patients (CRF), acquired
 XX immunodeficiency syndrome (AIDS) and for treating cancer patients
 XX undergoing chemotherapy. It is also useful for treating patients by
 XX stimulating the division and differentiation of committed erythroid
 XX progenitors in the bone marrow
 XX Sequence 201 AA;

Query Match 96.3%; Score 861; DB 5; Length 201;
 Best Local Similarity 97.1%; Pred. No. 1.8e-87;
 Matches 169; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 APPRIEGRAPPRILICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPTKVNFAWK 60
 DB 28 APFGAAHYAPPRILICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPTKVNFAWK 87
 QY 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLRAL 120
 DB 88 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLRAL 147
 QY 121 GAOKEAISPPDAASAAPLRTITADTFKLFVSVNFRGLKLYTGACRTGDR 174
 DB 148 GAOKEAISPPDAASAAPLRTITADTFKLFVSVNFRGLKLYTGACRTGDR 201

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RESULT 5
AAW33354
ID AAW33354 standard; protein; 412 AA.
XX AC AAW33354;
XX DT 24-FEB-1998 (first entry)
XX DE Oligopeptide GST-Epo.
XX KW Oligopeptide GST-Epo; target cell; transfection; retroviral vector;
XX KW gene therapy; cancer; viral disease; acquired immunodeficiency syndrome;
XX OS AIDS.
XX OS Synthetic.
XX PN WO9718318-A1.
XX PD 22-MAY-1997.
XX PF 07-NOV-1996; 96WO-JP003254.
XX PR 13-NOV-1995; 95JP-00294382.
XX PR 08-MAR-1996; 96JP-00051847.
XX PA (TAKI ) TAKARA SHUZO CO LTD.
XX PI Asada K, Uemori T, Ueno T, Koyama N, Hashino K, Kato I;
XX DR WPI; 1997-289294/26.
XX DR N-PSDB; AAT93979.
XX PT Method for increasing efficacy of gene transfer to target cell using
XX PT retrovirus - by infection of the target cell in the presence of a
XX PT substance which binds to the virus and a substance which binds to the
XX PT target cell.
XX PS Example 3; Page 146-148; 194pp; Japanese.
XX CC The present sequence is the oligopeptide GST-Epo, which was used in the
XX CC development of a novel method for increasing the efficiency of gene
XX CC introduction into a target cell using a retroviral vector. The method
XX CC comprises carrying out viral infection of the target cell in the presence
XX CC of a retrovirus and target cell binding substance or substances. The
XX CC method can be used to effectively introduce genes into target cells for
XX CC the gene therapy of cancer and viral diseases, e.g. AIDS
XX SQ Sequence 412 AA;
Query Match 96.1%; Score 859; DB 2; Length 412;
Best Local Similarity 93.4%; Pred. No. 8.8e-87;
Matches 171; Conservative 2; Mismatches 0; Indels 10; Gaps 2;
QY 2 PPR---IEGR-----APRLICDSRVLEKAEENITTCGAHCSLNENITVPD 51
DB 216 PPSDLIEGGIFPNSGAPRLICDSRVLEKAEENITTCGAHCSLNENITVPD 275
QY 52 TKVNFYAWKMEVQQAVVWQGLALISEAVLRQALLVNSSQPWEPLQLHVDKAVSGLR 111
DB 276 TKVNFYAWKMEVQQAVVWQGLALISEAVLRQALLVNSSQPWEPLQLHVDKAVSGLR 335
QY 112 SLTLLRALGAQKEAISPDAASAPLRTITADTFRKLFVYSNFKLGLKLYTGEACRT 171
DB 336 SLTLLRALGAQKEAISPDAASAPLRTITADTFRKLFVYSNFKLGLKLYTGEACRT 395
QY 172 GDR 174
DB 396 GDR 398
RESULT 6

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ABW77899
ID ABB77899 standard; protein; 169 AA.
XX AC ABB77899;
XX DT 07-OCT-2002 (first entry)
XX DE Amino acid sequence of a modified human erythropoietin (EPO).
XX KW Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
XX KW red blood cell production; anaemia; chronic renal failure;
XX KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
XX KW committed erythroid progenitor.
XX OS Synthetic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Cleavage-site 1..3
XX FT /note= "proteolytic cleavage site"
XX FT Protein 4..174
XX FT /note= "EPO protein"
XX PN WO200249673-A2.
XX PD 27-JUN-2002.
XX PF 08-DEC-2001; 2001WO-EPO14434.
XX PR 20-DEC-2000; 2000EP-00127891.
XX PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PI Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
XX PI Wozny M;
XX DR WPI; 2002-566640/60.
XX PT Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
XX PT useful for treating diseases correlated with anemia in chronic renal
XX PT failure patients and acquired immunodeficiency syndrome.
XX PS Disclosure; Page 39; 40pp; English.
XX CC The present sequence represents a modified human erythropoietin (EPO)
XX CC protein. The EPO was extended at the N-terminal by a proteolytic cleavage
XX CC site. It was used to produce conjugates of the invention. The
XX CC specification describes a conjugate comprising an EPO glycoprotein having
XX CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
XX CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
XX CC or a rearrangement of a glycosylation site). The glycoprotein is
XX CC covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
XX CC has in vivo biological activity of causing bone marrow cells to increase
XX CC production of reticulocytes and red blood cells. The conjugate increased
XX CC circulating half-life and plasma residence time, decreased clearance,
XX CC increased clinical activity in vivo, improved potency and stability, when
XX CC compared to unmodified EPO. The EPO conjugate is useful for preparing
XX CC medicaments for the treatment and prophylaxis of diseases correlated with
XX CC anaemia in chronic renal failure patients (CRF), acquired
XX CC immunodeficiency syndrome (AIDS) and for treating cancer patients
XX CC undergoing chemotherapy. It is also useful for treating patients by
XX CC stimulating the division and differentiation of committed erythroid
XX CC progenitors in the bone marrow
XX SQ Sequence 169 AA;
Query Match 95.8%; Score 856.5; DB 5; Length 169;
Best Local Similarity 97.1%; Pred. No. 4.6e-87;
Matches 169; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
QY 1 APPRIEGRAPRLICDSRVLEKAEENITTCGAHCSLNENITVPDKVNFYAWK 60
DB 1 APP-----APRLICDSRVLEKAEENITTCGAHCSLNENITVPDKVNFYAWK 55

```


The present sequence represents a modified human erythropoietin (EPO) protein. The EPO was extended at the N-terminal by a proteolytic cleavage site. It was used to produce conjugates of the invention. The specification describes a conjugate comprising an EPO glycoprotein having an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its analogues (where hEPO is modified by addition of 1-6 glycosylation sites or a rearrangement of a glycosylation site). The glycoprotein is covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein has *in vivo* biological activity of causing bone marrow cells to increase production of reticulocytes and red blood cells. The conjugate increased circulating half-life and plasma residence time, decreased clearance, increased clinical activity *in vivo*, improved potency and stability, when compared to unmodified EPO. The EPO conjugate is useful for preparing medicaments for the treatment and prophylaxis of diseases correlated with anaemia in chronic renal failure patients (CRF), acquired

Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RAPPRILCDRVLRYLLEKEAENITTCAGHCSSLNENITVPDVKVNFYAWKRMVGGQ 67
 DB 1 RAPPRILCDRVLRYLLEKEAENITTCAGHCSSLNENITVPDVKVNFYAWKRMVGGQ 60
 QY 68 AVEVWQGLALLSAVLRGOALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAI 127
 DB 61 AVEVWQGLALLSAVLRGOALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAI 120
 QY 128 SPDDAASAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGDR 174
 DB 121 SPDDAASAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGDR 167

RESULT 9
 ABU64199
 ID ABU64199 standard; protein; 425 AA.
 XX
 AC ABU64199;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Plasmid pED-dC-EpoFc Kbsignal peptide/EPO/Fcgammal insert protein.
 XX
 DE Trans epithelial systemic delivery; therapeutic delivery; aerosol;
 KW FcRn binding partner; lung.
 KW
 XX Synthetic.
 XX
 XX WO2003077834-A2.
 PN
 XX
 PD 25-SEP-2003.
 XX
 XX 03-JUL-2002; 2002WO-US021335.
 XX
 XX 15-MAR-2002; 2002US-0364482P.
 PR
 XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 PA
 XX Blumberg RS, Lencer WI, Simister NE, Bitonti AJ;
 PI
 XX WPI; 2003-767442/72.
 DR
 DR N-PSDB; AAL56122.
 XX
 XX Aerosol useful for systemic delivery of a therapeutic agent e.g.
 PT erythropoietin, growth hormone, interferon-alpha, or interferon-beta,
 PT comprises a conjugate of the agent and neonatal epithelial receptor-
 PT binding partner.
 XX
 XX Example 4; Fig 4B; Opp; English.
 XX
 XX The present invention relates to an aerosol which comprises a conjugate
 CC of a therapeutic agent and neonatal Fc receptor (FcRn) binding partner.
 CC The particles in the aerosol have a mass median aerodynamic diameter
 CC (MMAD) of at least 3 micro m. The aerosol can be used for the systemic
 CC delivery of a therapeutic agent (e.g. antigen (e.g. tumour antigen),
 CC polypeptide, oligonucleotide (e.g. antisense oligonucleotide),
 CC erythropoietin, growth hormone, interferon-alpha, interferon-beta and
 CC follicle stimulating hormone). The present sequence is a protein used in
 CC the exemplification of the invention
 XX
 XX Sequence 425 AA;
 SQ

Query Match 95.6%; Score 855; DB 7; Length 425;
 Best Local Similarity 97.7%; Pred. NO. 2.6e-86;
 Matches 167; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 RIEGRAPRLICDRVLRYLLEKEAENITTCAGHCSSLNENITVPDVKVNFYAWKRM 63
 DB 20 RAGSRAPRLICDRVLRYLLEKEAENITTCAGHCSSLNENITVPDVKVNFYAWKRM 79
 QY 64 VGGQAVEVWQGLALLSAVLRGOALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQ 123

DB 80 VGGQAVEVWQGLALLSAVLRGOALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQ 139
 QY 124 KEAISPPDAASAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGDR 174
 DB 140 KEAISPPDAASAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGDR 190

RESULT 10
 ADO10511
 ID ADO10511 standard; protein; 425 AA.
 XX
 AC ADO10511;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 XX Kb signal peptide/EPO/IgG1 Fc fragment fusion protein, SEQ ID NO:8.
 DE
 XX Drug delivery; aerosol; transepithelial; FcRn ligand;
 KW neonatal Fc receptor; central airway epithelium; lung; antigen;
 KW tumour antigen; erythropoietin; EPO; growth hormone; interferon-alpha;
 KW IFN-alpha; interferon-beta; IFN-beta; follicle stimulating hormone; FSH;
 KW therapeutic antibody; CAMPATH; SIMULACT; ZENAPAX; REMICADE; HUMIRA;
 KW SYNAGIS; RITUXAN; HERCEPTIN; CEA-CIDE; pneumonia; lung cancer;
 KW extranodal pulmonary non-Hodgkin's lymphoma; allograft rejection;
 KW autoimmune disease; rheumatoid arthritis; Crohn's disease; antirheumatic;
 KW antiarthritic; cytostatic; antiinflammatory; immunotherapy; vaccine;
 KW human; immunoglobulin G1; IgG1 Fc fragment; Fc-gamma-1;
 KW Kb signal peptide; fusion protein; plasmid pED-dC-EpoFc.
 XX
 XX Homo sapiens.
 OS
 OS Chimeric.
 OS Synthetic.
 XX

Key Location/Qualifiers
 Peptide 1..21 /label= Kb_signal_peptide
 Peptide 22..24 /note= "3 residue peptide linker"
 Protein 25..425 /note= "EPO/IgG1 Fc fragment fusion protein"
 Region 25..190 /note= "Human mature EPO"
 Region 191..198 /note= "8 residue peptide linker (SEQ ID NO:27)"
 Region 199..425 /note= "IgG1 Fc fragment_ (SEQ ID NO:2)"
 XX
 XX WO2004004798-A2.
 XX
 XX 15-JAN-2004.
 XX
 XX 09-MAY-2003; 2003WO-US014428.
 XX
 XX 03-JUL-2002; 2002WO-US021335.
 XX
 XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 PA (UYBR-) UNIV BRANDEIS.
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 PA (SYNT-) SYNTONIX PHARM INC.
 XX
 XX Blumberg RS, Lencer WI, Simister NE, Bitonti AJ;
 PI
 XX WPI; 2004-099348/10.
 DR N-PSDB; ADO10510.
 XX
 XX Systemic delivery of therapeutic agent involves administering effective
 PT amount of aerosol of therapeutic agent and neonatal Fc receptor (FcRn)
 PT binding partner to lung.
 XX
 XX Example 4; SEQ ID NO 8; 122pp; English.
 PS
 XX The invention relates to a method for the transepithelial systemic
 CC

delivery of a therapeutic agent. The method involves administering an effective amount of an aerosol of a therapeutic agent (especially an antibody) and a neonatal Fc receptor (FcRn) binding partner to the lungs such that a central lung zone/peripheral lung zone deposition ratio (C/P ratio) is 0.7 or more. Human FcRn is expressed in adult epithelial tissues, and provides a receptor-specific mechanism for transport across an epithelial barrier. Its expression has been found to be more extensive in central airways than in the periphery of the lung. The invention also relates to an aerosol of a conjugate of a therapeutic agent and an FcRn binding partner, where the aerosol particles have a mass median aerodynamic diameter (MMAD) of 3 micrometres or more; an aerosol delivery system; and a method for its manufacture. The method can be used to administer a wide variety of therapeutic agents to central airway epithelium. Such therapeutic agents include oligonucleotides (including antisense oligonucleotides) or proteins such as antigens (especially tumour antigens), erythropoietin (EPO), growth hormone, interferon-alpha (IFN-alpha), interferon-beta (IFN-beta), follicle stimulating hormone (FSH) and especially therapeutic or diagnostic antibodies. Therapeutic antibodies that may be administered using the method of the invention comprise those targeted to CD52, CD25, TNF-alpha, respiratory syncytial virus (RSV), CD20, HER2 or CEA, selected from CAMPATH, SIMULACT, ZENAPAX, REMICADE, HUMIRA, SYNAGIS, RITUXAN, HERCETIN and CEA-CIDE. Therapeutics administered using the method of the invention may be used to treat deep lung diseases such as RSV pneumonia, cytomegalovirus (CMV) pneumonia, primary and metastatic lung cancer, and extranodal pulmonary non-Hodgkin's lymphoma; extrapulmonary diseases such as cancer and allograft rejection; and autoimmune diseases chosen from rheumatoid arthritis and Crohn's disease. The present sequence represents a fusion protein comprising the Kb signal peptide, human EPO and the human IgG1 Fc fragment (Fc-gamma-1), which is encoded by plasmid pED.dC.Epofc.

XX Sequence 425 AA;

Query Match 95.6%; Score 855; DB 8; Length 425;
Best Local Similarity 97.7%; Pred. No. 2.6e-86;
Matches 167; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 RIGRAPPRLICDSRVLLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWKME 63
DB 20 RAGSRAPPRLICDSRVLLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWKME 79

QY 64 VGOQAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQ 123
DB 80 VGOQAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQ 139

QY 124 KEAISPPDAASAAPLRTITADTPRKLFRVYSNPLRGKLYTGEACRTGDR 174
DB 140 KEAISPPDAASAAPLRTITADTPRKLFRVYSNPLRGKLYTGEACRTGDR 190

RESULT 11
ADJ71846
ID ADJ71846 standard; protein; 205 AA.

XX ADJ71846;

XX 06-MAY-2004 (first entry)

DE Non-glycosylated EPO analogue with modified protease B signal peptide.

XX non-glycosylated erythropoietin analogue; EPO analogue; PEG; anaemia;
XX protease B signal peptide.

OS Chimeric.

OS Synthetic.

OS Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 1..39 /note= "Modified protease B signal peptide region"

FT Misc-difference 40..205

XX /note= "Non-glycosylated EPO analogue region"

PN WO2004009627-A1.
XX 29-JAN-2004.
PD 17-JUL-2003; 2003WO-CA001020.
PF 19-JUL-2002; 2002US-0396750P.
PR (CANG-) CANGENE CORP.

XX Cossar JD, Malek LT, Stewart DIH;
PI WPI; 2004-2143326/20.
XX N-PSDB; ADJ71845.

XX A non-glycosylated erythropoietin (EPO) analog useful treating anemia,
XX where the lysine at position 45 and/or 116 has been replaced with an
XX amino acid that cannot be pegylated.

XX Disclosure; SEQ ID NO 29; 74pp; English.

XX The invention comprises the amino acid and coding sequences of non-
XX glycosylated erythropoietin (EPO) analogues, where the lysine at position
XX 45 and/or 116 has been replaced with an amino acid that cannot be
XX pegylated. The non-glycosylated EPO analogues of the invention are useful
XX for treating anaemia. The present amino acid sequence represents a non-
XX glycosylated EPO analogue with a modified protease B signal peptide.
XX NOTE: The present sequence is included in the sequence listing as SEQ ID
XX No 29, however another sequence on page 28 of the specification is also
XX shown as SEQ ID No 29.

XX Sequence 205 AA;

Query Match 95.5%; Score 854; DB 8; Length 205;
Best Local Similarity 96.6%; Pred. No. 1.2e-86;
Matches 168; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APPRIEGRAPPRLICDSRVLLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWK 60
DB 32 AVPTAAAAAPRRLICDSRVLLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWK 91

QY 61 RMEVGQAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRAL 120
DB 92 RMEVGQAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRAL 151

QY 121 GAKQEAISPPDAASAAPLRTITADTPRKLFRVYSNPLRGKLYTGEACRTGDR 174
DB 152 GAKQEAISPPDAASAAPLRTITADTPRKLFRVYSNPLRGKLYTGEACRTGDR 205

RESULT 12
AAP70398
ID AAP70398 standard; protein; 166 AA.

XX AAP70398;

XX 19-FEB-1991 (first entry)

DE Sequence of human erythropoietin (EPO).

XX Mega-karyocyte-platelet growth factor; hormone;
XX mega-karyocyte colony stimulating factor; therapy;
XX small acetyl cholinesterase positive cell; erythrocyte growth effect.

OS Homo sapiens.

XX JP62149624-A.

XX 03-JUL-1987.

XX 15-AUG-1986; 86JP-00191542.

XX 13-SEP-1985; 85JP-00203049.

XX (KAWA/) KAWAKITA M.
 PA WPI; 1987-224837/32.
 DR
 XX
 PT Megakaryocyte-platelet growth factor - contains as active component human
 PT erythropoietin and is used to treat diseases caused by decrease in
 PT platelets.
 XX
 XX Disclosure; Page 181; 8pp; Japanese.
 XX
 XX All of the Cys residues in the SQ are labelled "SH". Megakaryocyte-
 CC platelet growth factor contains human EPO as an active principle. Human
 CC EPO has a megakaryocyte colony-stimulating activity and increases the
 CC ratio of small acetyl cholinesterase positive cell (SachR+) which is
 CC immature megakaryocyte. Human EPO effects megakaryocyte-platelet system
 CC other than an erythrocyte growth effect. Megakaryocyte-platelet growth is
 CC usable as a remedy for diseases caused by a platelet decrease
 XX
 SQ Sequence 166 AA;

Query Match 95.2%; Score 851; DB 1; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.8e-86;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 APPRLICDSRVLERYLLEAKEAENITTCGAHCNLENITVPTKYNFYAWKMEVGGQA 68
 DB 1 APPRLICDSRVLERYLLEAKEAENITTCGAHCNLENITVPTKYNFYAWKMEVGGQA 60
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
 DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
 QY 129 PPDAASAAPLRTITADTFKLFVYSNFLRGKLYTGACRTGDR 174
 DB 121 PPDAASAAPLRTITADTFKLFVYSNFLRGKLYTGACRTGDR 166

RESULT 13
 AAR23593
 ID AAR23593 standard; protein; 166 AA.

AC AAR23593;
 XX
 DT 20-OCT-1992 (first entry)
 XX
 DE Recombinant hematopoietic molecule portion 2.
 XX
 KW Erythropoietin; EPO; erythrocytes; IL-3; haematopoiesis.
 XX
 OS Homo sapiens.
 XX
 PN WO9206116-A.
 XX
 PD 16-APR-1992.
 XX
 PF 26-SEP-1991; 91WO-US007053.
 XX
 PR 28-SEP-1990; 90US-00589958.
 XX
 XX (ORTH) ORTHO PHARM CORP.
 PA
 XX Rosen JI;
 PI
 XX WPI; 1992-150819/18.
 DR
 XX Recombinant haematopoietic molecules useful in treating anaemia(s) -
 PT comprise IL3 or GM-CSF and EPO, G-CSF, IL-5 or M-CSF and has early and
 PT later myeloid differentiation activity.
 XX
 XX Disclosure; Page 32; 82pp; English.
 PS
 XX This protein sequence given comprises the entire amino acid sequence of
 CC

CC human erythropoietin (EPO). EPO leads to the maturation of erythrocytes
 CC and is therefore designated as a late myeloid differentiation factor
 CC (MDF). Within the scope of the invention hybrid molecules were produced
 CC which contain at least a portion of an early MDF and at least a portion
 CC of a late MDF covalently linked. The EPO sequence given is effective
 CC within the scope of the invention in full or in a truncated version.
 CC Amino acids 7-161 act as a late MDF when recombined with an early MDF eg.
 CC IL-3. These compounds can be used to promote haematopoiesis in a patient.
 CC The bonding of the early and late factors allows a very high conc. of
 CC late MDF at the surface of a cell which the early MDF is bound. It also
 CC allows the early MDA to act more specifically to stimulate only the
 CC desired lineage, thus reducing undesirable effects. These compounds are
 CC useful for treating anaemias of various origins eg. renal failure and
 CC AIDS. It is easier to produce and administer one recombinant molecule
 CC rather than two separate molecules
 XX

SQ Sequence 166 AA;

Query Match 95.2%; Score 851; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.8e-86;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 APPRLICDSRVLERYLLEAKEAENITTCGAHCNLENITVPTKYNFYAWKMEVGGQA 68
 DB 1 APPRLICDSRVLERYLLEAKEAENITTCGAHCNLENITVPTKYNFYAWKMEVGGQA 60
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
 DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
 QY 129 PPDAASAAPLRTITADTFKLFVYSNFLRGKLYTGACRTGDR 174
 DB 121 PPDAASAAPLRTITADTFKLFVYSNFLRGKLYTGACRTGDR 166

RESULT 14
 AAW58404

ID AAW58404 standard; protein; 166 AA.

AC AAW58404;
 XX
 DT 12-OCT-1998 (first entry)
 XX
 DE Human erythropoietin.
 XX
 KW Erythropoietin receptor agonist; EPO; human; anaemia;
 KW haematopoietic deficiency; red blood cell; erythroid progenitor;
 KW bone marrow suppression.
 XX
 OS Homo sapiens.
 XX
 PN WO9818926-A1.
 XX
 PD 07-MAY-1998.
 XX
 PF 23-OCT-1997; 97WO-US018703.
 XX
 PR 25-OCT-1996; 96US-0034044P.
 XX
 XX (SEAR) SEARLE & CO G D.
 PA
 XX McWherter CA, Feng Y, Summers N;
 PI
 XX WPI; 1998-272221/24.
 DR
 DR N-PSDB; AAV31031.
 XX
 XX Human erythropoietin receptor agonist polypeptide - used to stimulate the
 PT production of red blood cells in a patient.
 PT
 XX
 XX Claim 1; Page 93; 112pp; English.
 PS
 XX A claimed human erythropoietin (EPO) receptor agonist polypeptide
 CC comprises a modified EPO amino acid sequence given in AAW58404, where (a)
 CC

CC optionally 1-6 amino acids from the N-terminus and 1-5 from the C-terminus can be deleted, (b) the N-terminus is joined to the C-terminus directly or through a linker (see AA58405-12) capable of joining the N-terminus to the C-terminus, (c) there are new C- and N-termini at any two consecutive amino acids from amino acids 23-24 to 38-39, 40-41 to 41-42, 43-44 to 48-49, 50-51 to 57-58, 77-78 to 82-83, 84-85 to 88-89, and 108-109 to 131-132, and (d) optionally the agonist polypeptide is preceded by Met, Ala, or Met-Ala. 60 Of these circularly permuted EPO receptor agonists (see AA58413-72) are claimed. Also claimed are: nucleic acid molecules (see AA590971-V21030) encoding novel EPO receptor agonists; a method of producing an EPO receptor agonist using transformed or transfected host cells; and methods for stimulating the production of haematopoietic cells, for selective ex vivo expansion of erythroid progenitors, and treating patients having a haematopoietic disorder using the EPO receptor agonists. The EPO receptor agonists retain one or more activities of native EPO and may also show improved haematopoietic cell-stimulating activity and/or an improved activity profile which may include reduction of undesirable biological activities associated with native EPO and/or have improved physical properties such as increased solubility, stability and refold efficiency

XX Sequence 166 AA;

Query Match 95.2%; Score 851; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.8e-86;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYLEAKEAENITTCGAHCSLNENITVPDTKVNFAWKMEVQQA 68
 Db 1 APRRLICDSRVLYLEAKEAENITTCGAHCSLNENITVPDTKVNFAWKMEVQQA 60

QY 69 VEVWQGLALLSEAVLHGQALLVNSQWPEQLHVDKAVSGLSLTLLRALGQAEKIS 128
 Db 61 VEVWQGLALLSEAVLHGQALLVNSQWPEQLHVDKAVSGLSLTLLRALGQAEKIS 120

QY 129 PPDAASAPLRTITADTFKLFVNSFLRGLKLYTGEACRTGDR 174
 Db 121 PPDAASAPLRTITADTFKLFVNSFLRGLKLYTGEACRTGDR 166

RESULT 15
 AA777780
 ID AA777780 standard; protein; 166 AA.

AC AA777780;
 XX
 DT 24-NOV-1998 (first entry)
 XX
 DE Human EPO receptor agonist polypeptide.

KW Haematopoietic receptor agonist; erythropoietin receptor agonist; EPO;
 KW human; chimeric protein; stem cell expansion; tumour; infection;
 KW autoimmune disease; haematopoietic disorder; therapy; dendritic cell.

XX Homo sapiens.

EH Key Location/Qualifiers
 FT Misc-difference 1..6
 FT /note= "1-6 amino acids of the N-terminus are optionally deleted"
 FT Misc-difference 23..24
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 24..25
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 25..26
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 26..27
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 27..28
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 28..29
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 29..30
 FT /note= "possible positions of new C- and N-termini"

FT Misc-difference 30..31
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 31..32
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 32..33
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 33..34
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 34..35
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 35..36
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 36..37
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 37..38
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 38..39
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 39..40
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 40..41
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 41..42
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 42..43
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 43..44
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 44..45
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 45..46
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 46..47
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 47..48
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 48..49
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 49..50
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 50..51
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 51..52
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 52..53
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 53..54
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 FT Misc-difference 55..56
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 FT Misc-difference 56..57
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 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 57..78
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 78..79
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 79..80
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 81..82
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 82..83
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 84..85
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 85..86
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 86..87
 FT /note= "possible positions of new C- and N-termini"

FT Misc-difference 87. .88 /note="possible positions of new C- and N-termini"
 FT Misc-difference 88. .89 /note="possible positions of new C- and N-termini"
 FT Misc-difference 108. .109 /note="possible positions of new C- and N-termini"
 FT Misc-difference 109. .110 /note="possible positions of new C- and N-termini"
 FT Misc-difference 110. .111 /note="possible positions of new C- and N-termini"
 FT Misc-difference 111. .112 /note="possible positions of new C- and N-termini"
 FT Misc-difference 112. .113 /note="possible positions of new C- and N-termini"
 FT Misc-difference 113. .114 /note="possible positions of new C- and N-termini"
 FT Misc-difference 114. .115 /note="possible positions of new C- and N-termini"
 FT Misc-difference 115. .116 /note="possible positions of new C- and N-termini"
 FT Misc-difference 116. .117 /note="possible positions of new C- and N-termini"
 FT Misc-difference 117. .118 /note="possible positions of new C- and N-termini"
 FT Misc-difference 118. .119 /note="possible positions of new C- and N-termini"
 FT Misc-difference 119. .120 /note="possible positions of new C- and N-termini"
 FT Misc-difference 120. .121 /note="possible positions of new C- and N-termini"
 FT Misc-difference 121. .122 /note="possible positions of new C- and N-termini"
 FT Misc-difference 122. .123 /note="possible positions of new C- and N-termini"
 FT Misc-difference 123. .124 /note="possible positions of new C- and N-termini"
 FT Misc-difference 124. .125 /note="possible positions of new C- and N-termini"
 FT Misc-difference 125. .126 /note="possible positions of new C- and N-termini"
 FT Misc-difference 126. .127 /note="possible positions of new C- and N-termini"
 FT Misc-difference 127. .128 /note="possible positions of new C- and N-termini"
 FT Misc-difference 128. .129 /note="possible positions of new C- and N-termini"
 FT Misc-difference 129. .130 /note="possible positions of new C- and N-termini"
 FT Misc-difference 130. .131 /note="possible positions of new C- and N-termini"
 FT Misc-difference 131. .132 /note="possible positions of new C- and N-termini"
 FT Misc-difference 162. .166 /note="possible positions of new C- and N-termini"
 FT Misc-difference 162. .166 /note="1-5 amino acids of the C-terminus are optionally deleted"
 XX
 DN WO9817810-A2.
 XX
 XX 30-APR-1998.
 XX
 XX 23-OCT-1997; 97WO-US020037.
 XX
 XX 25-OCT-1996; 96US-0029629P.
 XX
 XX (SEAR) SEARLE & CO G D.
 XX
 XX McWherter CA, Feng Y, McKearn JP, Summers NL, Staten NR;
 PI Streeter PR, Minnerly JC, Minster NI, Woulfe SL;
 XX
 XX WFI; 1998-261504/23.
 XX
 XX Multi-functional chimeric haematopoietic receptor agonist - useful to
 PT treat haematopoietic disorders, tumours, infections or autoimmune

PT diseases.
 XX Claim 1; Page 762; 841pp; English.
 XX
 CC A human erythropoietin (EPO) receptor agonist polypeptide comprises a
 CC modified EPO amino acid sequence of the formula provided in AAW77780, in
 CC which the N-terminus is joined to the C-terminus directly or via a
 CC linker, the polypeptide having new C- and N-termini at one of the
 CC positions indicated. Novel claimed multi-functional chimeric
 CC haematopoietic receptor agonists (see AAW77812-22) have the formula R1-L1
 CC -R2, R2-L1-R1, R1-R2 or R2-R1, where L is a linker and R1 and R2 are
 CC independently selected from: (a) the human EPO receptor agonist; (b) a
 CC human stem cell factor receptor agonist polypeptide (see AAW77781); (c) a
 CC human fit-3 receptor agonist polypeptide (see AAW77782); (d) a modified
 CC human granulocyte colony stimulating factor (G-CSF) polypeptide (see
 CC AAW77783); (e) modified human interleukin-3 polypeptide (see AAW77784);
 CC (f) modified human c-mpl ligand polypeptide (see AAW77785); and (g) a
 CC factor selected from the group consisting of a CSF, a cytokine, a
 CC lymphokine, an interleukin and a haematopoietic growth factor, provided
 CC that at least R1 or R2 is selected from (a), (b) or (c) as above. The
 CC multi-functional chimeric haematopoietic receptor agonist can be used to
 CC stimulate the production of haematopoietic cells in a patient, for the ex
 CC vivo expansion of haematopoietic cells, for the production of dendritic
 CC
 Query Match 95.2%; Score 851; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.8e-86;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 APRRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPTKYNFYAWKMEVGOQA 68
 DB 1 APRRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPTKYNFYAWKMEVGOQA 60
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDKAVSGLSLTLRLALCAQKEAIS 128
 DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDKAVSGLSLTLRLALCAQKEAIS 120
 QY 129 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGDR 174
 DB 121 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGDR 166
 Search completed: November 19, 2004, 21:05:44
 Job time : 64.2534 secs

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OM protein - protein search, using sw model

Run on: November 19, 2004, 21:00:09 ; Search time 17.8375 Seconds
(without alignments)
646.913 Million cell updates/sec

Title: US-10-014-363-3

Perfect score: 894

Sequence: 1 APPRIEGRAPPLICDSRVL.....NFLRGKLYTGACRTGDR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	859	96.1	412	4	US-09-366-009-34
2	859	96.1	412	4	US-08-809-156B-34
3	851	95.2	166	1	US-08-318-193-70
4	851	95.2	166	3	US-09-604-871-2
5	851	95.2	166	4	US-09-604-938-2
6	851	95.2	166	4	US-09-462-941-2
7	851	95.2	166	5	PCT-US94-04361-37
8	851	95.2	193	1	US-07-903-220-1
9	851	95.2	193	2	US-08-883-795A-34
10	851	95.2	193	4	US-09-552-265B-4
11	846	94.6	165	3	US-09-604-871-1
12	846	94.6	165	4	US-09-604-938-1
13	846	94.6	165	4	US-09-830-967-1
14	843	94.3	165	4	US-09-554-451-8
15	843	94.3	193	4	US-09-552-265B-2
16	839	93.8	193	4	US-09-552-265B-5
17	835	93.4	166	5	PCT-US94-04361-45
18	830	92.8	166	4	US-09-552-265B-30
19	830	92.8	193	4	US-09-552-265B-46
20	829	92.7	166	4	US-09-552-265B-22
21	829	92.7	166	4	US-09-552-265B-32
22	829	92.7	193	4	US-09-552-265B-38
23	829	92.7	193	4	US-09-552-265B-48
24	827	92.5	166	4	US-09-552-265B-20
25	827	92.5	166	4	US-09-552-265B-24
26	827	92.5	193	4	US-09-552-265B-36
27	827	92.5	193	4	US-09-552-265B-40

28 826 92.4 166 4 US-09-552-265B-26 Sequence 26, Appl
29 826 92.4 166 4 US-09-552-265B-31 Sequence 31, Appl
30 826 92.4 193 4 US-09-552-265B-42 Sequence 42, Appl
31 826 92.4 193 4 US-09-552-265B-47 Sequence 47, Appl
32 825 92.3 166 4 US-09-552-265B-18 Sequence 18, Appl
33 825 92.3 166 4 US-09-552-265B-23 Sequence 23, Appl
34 825 92.3 166 4 US-09-552-265B-28 Sequence 28, Appl
35 825 92.3 166 4 US-09-552-265B-33 Sequence 33, Appl
36 825 92.3 193 4 US-09-552-265B-34 Sequence 34, Appl
37 825 92.3 193 4 US-09-552-265B-39 Sequence 39, Appl
38 825 92.3 193 4 US-09-552-265B-44 Sequence 44, Appl
39 825 92.3 193 4 US-09-552-265B-49 Sequence 49, Appl
40 823 92.1 166 4 US-09-552-265B-21 Sequence 21, Appl
41 823 92.1 166 4 US-09-552-265B-25 Sequence 25, Appl
42 823 92.1 193 4 US-09-552-265B-37 Sequence 37, Appl
43 823 92.1 193 4 US-09-552-265B-41 Sequence 41, Appl
44 822 91.9 166 4 US-09-552-265B-27 Sequence 27, Appl
45 822 91.9 193 4 US-09-552-265B-43 Sequence 43, Appl

ALIGNMENTS

RESULT 1

US-09-366-009-34
; Sequence 34, Application US/09366009
; Patent No. 6426042
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Ueno, Takashi
; Koyama, No. 6426042uto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear


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; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-366-009-34

Query Match          96.1%; Score 859; DB 4; Length 412;
Best Local Similarity 93.4%; Pred. No. 1.1e-99;
Matches 171; Conservative 2; Mismatches 0; Indels 10; Gaps 2;

QY  2 PPR---IEGR-----APPLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVDP 51
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Db  216 PPKSDLIEGRGIPRNSGAPPLICDSRVLQRYLLEAKEAENITTCGAHCSLNENITVDP 275

QY  52 TKVNFYAWKMEVGGQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLOLHVDKAVSGLR 111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  276 TKVNFYAWKMEVGGQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLOLHVDKAVSGLR 335

QY  112 SLTTLRALGAQKEAISPPDAASAAPLRTITADTFKLFVYSNFLRGKLYTGEACRT 171
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Db  336 SLTTLRALGAQKEAISPPDAASAAPLRTITADTFKLFVYSNFLRGKLYTGEACRT 395

QY  172 GDR 174
    |||
Db  396 GDR 398

RESULT 2
US-08-809-156B-34
; Sequence 34, Application US/08090156B
; Patent No. 6472204
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; APPLICANT: Umori, Takashi
; APPLICANT: Ueno, Takashi
; APPLICANT: Koyama, No. 6472204uto
; APPLICANT: Hashino, Kimikazu
; APPLICANT: Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; TITLE OF INVENTION: CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,156B
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/03254
; FILING DATE: 07-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 13,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; LENGTH: 412 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-809-156B-34

Query Match          96.1%; Score 859; DB 4; Length 412;
Best Local Similarity 93.4%; Pred. No. 1.1e-99;
Matches 171; Conservative 2; Mismatches 0; Indels 10; Gaps 2;

QY  2 PPR---IEGR-----APPLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVDP 51
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Db  216 PPKSDLIEGRGIPRNSGAPPLICDSRVLQRYLLEAKEAENITTCGAHCSLNENITVDP 275

QY  52 TKVNFYAWKMEVGGQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLOLHVDKAVSGLR 111
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QY  112 SLTTLRALGAQKEAISPPDAASAAPLRTITADTFKLFVYSNFLRGKLYTGEACRT 171
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Db  336 SLTTLRALGAQKEAISPPDAASAAPLRTITADTFKLFVYSNFLRGKLYTGEACRT 395

QY  172 GDR 174
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Db  396 GDR 398

RESULT 3
US-08-318-193-70
; Sequence 70, Application US/08318193
; Patent No. 5641663
; GENERAL INFORMATION:
; APPLICANT: GARVIN, Robert T.
; APPLICANT: MALEK, Lawrence T.
; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
; TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,193
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,314
; FILING DATE:
; APPLICATION NUMBER: US 07/224,568
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 18740/116 CACO
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
US-08-318-193-70

Query Match
Best Local Similarity 95.2%; Score 851; DB 1; Length 166;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRLEAEAEENITGCAEHCSLNENITVPDTKVNIFYAKRMEVGGQA 68
DB 1 APPRLICDSRVLYRLEAEAEENITGCAEHCSLNENITVPDTKVNIFYAKRMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120

QY 129 PDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 174
DB 121 PDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 166

RESULT 4
US-09-604-871-2
; Sequence 2, Application US/09604871
; Patent No. 6340742
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Hilger, Bernd
; APPLICANT: Josel, Hans-Peter
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1098 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,871
; CURRENT FILING DATE: 2000-06-28
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/151,454
; PRIOR FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: 60/147,452
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/142,243
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-871-2

Query Match
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Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120

QY 129 PDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 174
DB 121 PDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 166

RESULT 5
US-09-604-938-2
; Sequence 2, Application US/09604938
; Patent No. 6583272
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,938
; CURRENT FILING DATE: 2000-06-27

; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-938-2

Query Match
Best Local Similarity 95.2%; Score 851; DB 4; Length 166;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRLEAEAEENITGCAEHCSLNENITVPDTKVNIFYAKRMEVGGQA 68
DB 1 APPRLICDSRVLYRLEAEAEENITGCAEHCSLNENITVPDTKVNIFYAKRMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120

QY 129 PDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 174
DB 121 PDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 166

RESULT 6
US-09-462-941-2
; Sequence 2, Application US/09462941
; Patent No. 6608183
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/09/462,941
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-462-941-2

Query Match
Best Local Similarity 95.2%; Score 851; DB 4; Length 166;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRLEAEAEENITGCAEHCSLNENITVPDTKVNIFYAKRMEVGGQA 68
DB 1 APPRLICDSRVLYRLEAEAEENITGCAEHCSLNENITVPDTKVNIFYAKRMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120

QY 129 PDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 174
DB 121 PDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 166

RESULT 7
PCT-US94-04361-37
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; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/903,220
; FILING DATE: 19920731
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: 1248/27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
; US-07-903-220-1
;
Query Match 95.2%; Score 851; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 3.3e-99;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 9 APPRLCDSRVRLRYLLEAKEARNITTCAGHCSLNENITVPDTKYNFYAWKMEVCGQA 68
DB 28 APPRLCDSRVRLRYLLEAKEARNITTCAGHCSLNENITVPDTKYNFYAWKMEVCGQA 87
;
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 128
DB 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 147
;
QY 129 PPDASAAPLRTITADTFKRLFRVYGNFLRGKULKYTGEACRTGDR 174
DB 148 PPDASAAPLRTITADTFKRLFRVYGNFLRGKULKYTGEACRTGDR 193
;
RESULT 9
US-08-883-795A-34
; Sequence 34, Application US/08883795A
; Patent No. 5985607
; GENERAL INFORMATION:
; APPLICANT: Delcuve, Genevieve
; APPLICANT: Awang, Gregor
; TITLE OF INVENTION: Recombinant DNA Molecules and Expression
; TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,795A
; FILING DATE: 27-JUN-1997

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/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Gravelle, Micheline
/ REGISTRATION NUMBER: 40,261
/ REFERENCE/DOCKET NUMBER: 7841-062
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (416) 364-7311
/ TELEFAX: (416) 361-1398
/ INFORMATION FOR SEQ ID NO: 34:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 193 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-883-795A-34

Query Match          95.2%; Score 851; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 3.3e-99;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRLLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 68
Db 28 APRLLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 87

QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
Db 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 147

QY 129 PPDASAAPLRTITADTFKRLFRVYSNFLRGKLYTGEACRTGDR 174
Db 148 PPDASAAPLRTITADTFKRLFRVYSNFLRGKLYTGEACRTGDR 193

RESULT 10
US-09-552-265B-4
/ Sequence 4, Application US/09552265B
/ Patent No. 6555343
/ GENERAL INFORMATION:
/ APPLICANT: DeSavage, Frederick
/ APPLICANT: Henner, Dennis, J.
/ TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
/ FILE OF INVENTION: polypeptides and nucleic acids encoding the same
/ FILE REFERENCE: GENENT.057CP1
/ CURRENT APPLICATION NUMBER: US/09/552,265B
/ CURRENT FILING DATE: 2000-04-19
/ PRIOR APPLICATION NUMBER: US 09/307307
/ PRIOR FILING DATE: 1999-05-17
/ NUMBER OF SEQ ID NOS: 49
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 193
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-552-265B-4

Query Match          95.2%; Score 851; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 3.3e-99;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRLLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 68
Db 28 APRLLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 87

QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
Db 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 147

QY 129 PPDASAAPLRTITADTFKRLFRVYSNFLRGKLYTGEACRTGDR 174
Db 148 PPDASAAPLRTITADTFKRLFRVYSNFLRGKLYTGEACRTGDR 193

RESULT 11
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US-09-604-871-1
/ Sequence 1, Application US/09604871
/ Patent No. 6340742
/ GENERAL INFORMATION:
/ APPLICANT: Burg, Josef
/ APPLICANT: Hilger, Bernd
/ APPLICANT: Josef, Hans-Peter
/ TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
/ FILE REFERENCE: 1098 nonprovisional
/ CURRENT APPLICATION NUMBER: US/09/604,871
/ CURRENT FILING DATE: 2000-06-28
/ PRIOR APPLICATION NUMBER: 60/151,454
/ PRIOR FILING DATE: 1999-08-30
/ PRIOR APPLICATION NUMBER: 60/147,452
/ PRIOR FILING DATE: 1999-08-05
/ PRIOR APPLICATION NUMBER: 60/142,243
/ PRIOR FILING DATE: 1999-07-02
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 165
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-604-871-1

Query Match          94.6%; Score 846; DB 3; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.1e-98;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRLLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 68
Db 1 APRLLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120

QY 129 PPDASAAPLRTITADTFKRLFRVYSNFLRGKLYTGEACRTGD 173
Db 121 PPDASAAPLRTITADTFKRLFRVYSNFLRGKLYTGEACRTGD 165

RESULT 12
US-09-604-938-1
/ Sequence 1, Application US/09604938
/ Patent No. 6583272
/ GENERAL INFORMATION:
/ APPLICANT: Bailon, Pascal
/ TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
/ FILE REFERENCE: 1097 nonprovisional
/ CURRENT APPLICATION NUMBER: US/09/604,938
/ CURRENT FILING DATE: 2000-06-27
/ PRIOR APPLICATION NUMBER: 60/166,151
/ PRIOR FILING DATE: 1999-11-17
/ PRIOR APPLICATION NUMBER: 60/151,548
/ PRIOR FILING DATE: 1999-08-13
/ PRIOR APPLICATION NUMBER: 60/150,225
/ PRIOR FILING DATE: 1999-08-23
/ PRIOR APPLICATION NUMBER: 60/142,254
/ PRIOR FILING DATE: 1999-07-02
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 165
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-604-938-1

Query Match          94.6%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.1e-98;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRLLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA 68
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Db 1 APPRLICDSRVLELYLEAKEAENITTCAGHCSLNENITVPTDKNFYAWKMEVGOQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 129 PPDASAAPLRTITADTFRKLFYVSNFLRGKLYTGEACRTGD 173
Db 121 PPDASAAPLRTITADTFRKLFYVSNFLRGKLYTGEACRTGD 165

RESULT 13

US-09-830-967-1
; Sequence 1, Application US/09830967
; Patent No. 6777205
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie No. 6777205th America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Host Cells Expressing Recombinant Human Erythropoietin
; FILE REFERENCE: 1909.0020002
; CURRENT APPLICATION NUMBER: US/09/830,967
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: AR 99-01-00679
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: AR 98-01-05609
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-967-1

Query Match 94.6%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.1e-98;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 APPRLICDSRVLELYLEAKEAENITTCAGHCSLNENITVPTDKNFYAWKMEVGOQA 68
Db 1 APPRLICDSRVLELYLEAKEAENITTCAGHCSLNENITVPTDKNFYAWKMEVGOQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 129 PPDASAAPLRTITADTFRKLFYVSNFLRGKLYTGEACRTGD 173
Db 121 PPDASAAPLRTITADTFRKLFYVSNFLRGKLYTGEACRTGD 165

RESULT 14

US-09-554-451-8
; Sequence 8, Application US/09554451
; Patent No. 6680207
; GENERAL INFORMATION:
; APPLICANT: Jonathan Paul MURPHY
; Anthony ATKINSON
; TITLE OF INVENTION: Detection of Molecules in Samples
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/554,451
; FILING DATE: 15-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/03449
; FILING DATE: No. 6680207ember 16, 1998
; APPLICATION NUMBER: GB 9723955.2
; FILING DATE: No. 6680207ember 14, 1997
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-554-451-8

Query Match 94.3%; Score 843; DB 4; Length 165;
Best Local Similarity 99.4%; Pred. No. 2.7e-98;
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 9 APPRLICDSRVLELYLEAKEAENITTCAGHCSLNENITVPTDKNFYAWKMEVGOQA 68
Db 1 APPRLICDSRVLELYLEAKEAENITTCAGHCSLNENITVPTDKNFYAWKMEVGOQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 129 PPDASAAPLRTITADTFRKLFYVSNFLRGKLYTGEACRTGD 173
Db 121 PPDASAAPLRTITADTFRKLFYVSNFLRGKLYTGEACRTGD 165

RESULT 15

US-09-552-265B-2
; Sequence 2, Application US/09552265B
; Patent No. 6555343
; GENERAL INFORMATION:
; APPLICANT: DeSauvage, Frederick
; APPLICANT: Henner, Dennis J
; TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
; FILE REFERENCE: GENENT.057CP1
; CURRENT APPLICATION NUMBER: US/09/552,265B
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: US 09/307307
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-09-552-265B-2

Query Match 94.3%; Score 843; DB 4; Length 193;
Best Local Similarity 99.4%; Pred. No. 3.4e-98;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 APPRLICDSRVLELYLEAKEAENITTCAGHCSLNENITVPTDKNFYAWKMEVGOQA 68
Db 28 APPRLICDSRVLELYLEAKEAENITTCAGHCSLNENITVPTDKNFYAWKMEVGOQA 87
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
Db 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 147
QY 129 PPDASAAPLRTITADTFRKLFYVSNFLRGKLYTGEACRTGD 174

Db 148 PPDASAAPLRTTITADTFKLFVYSNFLRGKLYTGEACRTGDR 193

Search completed: November 19, 2004, 21:13:01
Job time : 18.8375 secs

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OM protein - protein search, using sw model

Run on: November 19, 2004, 21:11:10 ; Search time 82.4565 Seconds
(without alignments)
747.281 Million cell updates/sec

Title: US-10-014-363-3

Perfect score: 894

Sequence: 1 APPRIEGRAPPLICDSRVLL.....NFLRGKLYTGACRTGDR 174

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Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	861	96.3	174	13	US-10-014-363-5
3	859	96.1	412	10	US-09-775-964-34
4	856.5	95.8	169	13	US-10-014-363-4
5	855	95.6	425	14	US-10-435-608-8
6	855	95.6	425	15	US-10-622-108-8
7	851	95.2	166	9	US-09-853-731-2
8	851	95.2	166	13	US-10-014-363-2
9	851	95.2	166	14	US-10-241-356-2
10	851	95.2	166	14	US-10-293-551-2
11	851	95.2	166	14	US-10-400-377-2
12	851	95.2	166	14	US-10-400-708-2
13	851	95.2	166	14	US-10-298-148-2
14	851	95.2	166	14	US-10-298-148-2
15	851	95.2	166	14	US-10-298-148-2
16	851	95.2	166	14	US-10-298-148-2
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29	851	95.2	166	14	US-10-298-148-2
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31	851	95.2	166	14	US-10-298-148-2
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34	851	95.2	166	14	US-10-298-148-2
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37	851	95.2	166	14	US-10-298-148-2
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39	851	95.2	166	14	US-10-298-148-2
40	851	95.2	166	14	US-10-298-148-2
41	851	95.2	166	14	US-10-298-148-2
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43	851	95.2	166	14	US-10-298-148-2
44	851	95.2	166	14	US-10-298-148-2
45	851	95.2	166	14	US-10-298-148-2

14	851	95.2	166	15	US-10-360-101-227	Sequence 227, App
15	851	95.2	166	15	US-10-467-115-1	Sequence 1, Appli
16	851	95.2	166	16	US-10-658-834A-201	Sequence 201, App
17	851	95.2	166	16	US-10-773-939-2	Sequence 2, Appli
18	851	95.2	166	16	US-10-774-149-2	Sequence 2, Appli
19	851	95.2	166	16	US-10-468-496-133	Sequence 133, App
20	851	95.2	166	17	US-10-773-654-2	Sequence 2, Appli
21	851	95.2	193	10	US-09-813-775C-4	Sequence 4, Appli
22	851	95.2	193	14	US-10-113-824-2	Sequence 2, Appli
23	851	95.2	193	16	US-10-612-665-10	Sequence 10, Appli
24	851	95.2	193	16	US-10-612-665-22	Sequence 22, Appli
25	851	95.2	193	16	US-10-612-665-112	Sequence 112, App
26	851	95.2	193	17	US-10-676-694-10	Sequence 10, Appli
27	851	95.2	193	17	US-10-676-694-22	Sequence 22, Appli
28	851	95.2	193	17	US-10-676-694-112	Sequence 112, App
29	851	95.2	428	14	US-10-435-608-10	Sequence 10, Appli
30	851	95.2	428	15	US-10-622-108-10	Sequence 10, Appli
31	849	95.0	166	16	US-10-658-834A-959	Sequence 959, App
32	849	95.0	166	16	US-10-658-834A-967	Sequence 967, App
33	848	94.9	166	16	US-10-658-834A-952	Sequence 952, App
34	848	94.9	166	16	US-10-658-834A-955	Sequence 955, App
35	848	94.9	166	16	US-10-658-834A-958	Sequence 958, App
36	848	94.9	166	16	US-10-658-834A-966	Sequence 966, App
37	848	94.9	193	14	US-10-435-608-4	Sequence 4, Appli
38	848	94.9	193	15	US-10-622-108-4	Sequence 4, Appli
39	848	94.9	193	16	US-10-612-665-63	Sequence 63, Appli
40	848	94.9	193	16	US-10-612-665-64	Sequence 64, Appli
41	848	94.9	193	16	US-10-612-665-70	Sequence 70, Appli
42	848	94.9	193	16	US-10-612-665-81	Sequence 81, Appli
43	848	94.9	193	16	US-10-612-665-88	Sequence 88, Appli
44	848	94.9	193	16	US-10-612-665-91	Sequence 91, Appli
45	848	94.9	193	17	US-10-676-694-63	Sequence 63, Appli

ALIGNMENTS

RESULT 1

US-10-014-363-3
; Sequence 3, Application US/10014363
; Publication No. US20020115833A1
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 174
; TYPE: PRT
; ORGANISM: CHO/dhfr-
US-10-014-363-3

Query Match 100.0%; Score 894; DB 13; Length 174;
Best Local Similarity 100.0%; Pred. No. 3.8e-90;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	APPRIEGRAPPLICDSRVLLRYLLEAKEAENITTCGAEHCSLNENITVPDTKVNFWYAWK 60
Db	1	APPRIEGRAPPLICDSRVLLRYLLEAKEAENITTCGAEHCSLNENITVPDTKVNFWYAWK 60
Qy	61	RMEVQQQAVEVWQGLALISEAVLRQALLVNSSQWPEPLQLHVDKAVSGLRSLTLLRAL 120
Db	61	RMEVQQQAVEVWQGLALISEAVLRQALLVNSSQWPEPLQLHVDKAVSGLRSLTLLRAL 120

QY 121 GAOKEAISPPDAASAPLRTITADTFRKLFRVYSNFRGLKLYTGEACRTGDR 174
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 Db 121 GAOKEAISPPDAASAPLRTITADTFRKLFRVYSNFRGLKLYTGEACRTGDR 174

RESULT 2

US-10-014-363-5
 ; Sequence 5, Application US/10014363
 ; Publication No. US20020115833A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burg, Josef
 ; APPLICANT: Engel, Alfred
 ; APPLICANT: Franze, Reinhard
 ; APPLICANT: Hilger, Bernd
 ; APPLICANT: Schurig, Hartmut Ernst
 ; APPLICANT: Tischer, Wilhelm
 ; APPLICANT: Wozny, Manfred
 ; TITLE OF INVENTION: Erythropoietin Conjugates
 ; FILE REFERENCE: Case 20805
 ; CURRENT APPLICATION NUMBER: US/10/014,363
 ; CURRENT FILING DATE: 2001-12-11
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 174
 ; TYPE: PRT
 ; ORGANISM: CHO/dhfr-
 US-10-014-363-5

Query Match 96.3%; Score 861; DB 13; Length 174;
 Best Local Similarity 97.1%; Pred. No. 1.7e-86;
 Matches 169; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 APPRIEGRAPPLICDSRVLERYLLLEAKEAENITTCGAHCNSLNENITVDPDTKVNFYAWK 60
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 Db 1 APPGAHYAPPLICDSRVLERYLLLEAKEAENITTCGAHCNSLNENITVDPDTKVNFYAWK 60
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 QY 61 RMEVGQAEVWQGLLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLLRAL 120
 |||||
 Db 61 RMEVGQAEVWQGLLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLLRAL 120
 |||||
 QY 121 GAOKEAISPPDAASAPLRTITADTFRKLFRVYSNFRGLKLYTGEACRTGDR 174
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 Db 121 GAOKEAISPPDAASAPLRTITADTFRKLFRVYSNFRGLKLYTGEACRTGDR 174

RESULT 3

US-09-775-964-34
 ; Sequence 34, Application US/09775964
 ; Publication No. US20030087437A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Asada, Kiyozo
 ; Uemori, Takashi
 ; Ueno, Takashi
 ; Koyama, No. US20030087437A1uto
 ; Hashino, Kimikazu
 ; Kato, Ikunoshin
 ; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
 CELLS WITH RETROVIRUS
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WEISER & ASSOCIATES
 ; STREET: 230 South Fifteenth Street, Suite 500
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/775,964
 ; FILING DATE: 20-Feb-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/366,009
 ; FILING DATE: 02-Aug-1999
 ; APPLICATION NUMBER: 08/809,156
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: JP 294382/1995
 ; FILING DATE: 13-NOV-1995
 ; APPLICATION NUMBER: JP 051847/1996
 ; FILING DATE: 08-MAR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Weiser, Gerard J.
 ; REGISTRATION NUMBER: 19,763
 ; REFERENCE/DOCKET NUMBER: 977.6507P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-875-8383
 ; TELEFAX: 215-875-8394
 ; INFORMATION FOR SEQ ID NO: 34:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 412 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
 ; US-09-775-964-34

Query Match 96.1%; Score 859; DB 10; Length 412;
 Best Local Similarity 93.4%; Pred. No. 9.1e-86;
 Matches 171; Conservative 2; Mismatches 0; Indels 10; Gaps 2;
 QY 2 PPR---IEGR-----APRLICDSRVLERYLLLEAKEAENITTCGAHCNSLNENITVDP 51
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 Db 216 PPKSDIIEGRGTPRNSGAPPLICDSRVLERYLLLEAKEAENITTCGAHCNSLNENITVDP 275
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 QY 52 TKNVFYAWKMEVGQAEVWQGLLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLR 111
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 Db 276 TKNVFYAWKMEVGQAEVWQGLLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLR 335
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 QY 112 SLTTLRALGAQKEAISPPDAASAPLRTITADTFRKLFRVYSNFRGLKLYTGEACRT 171
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 Db 336 SLTTLRALGAQKEAISPPDAASAPLRTITADTFRKLFRVYSNFRGLKLYTGEACRT 395
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 QY 172 GDR 174
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 Db 396 GDR 398

RESULT 4

US-10-014-363-4
 ; Sequence 4, Application US/10014363
 ; Publication No. US20020115833A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burg, Josef
 ; APPLICANT: Engel, Alfred
 ; APPLICANT: Franze, Reinhard
 ; APPLICANT: Hilger, Bernd
 ; APPLICANT: Schurig, Hartmut Ernst
 ; APPLICANT: Tischer, Wilhelm
 ; APPLICANT: Wozny, Manfred
 ; TITLE OF INVENTION: Erythropoietin Conjugates
 ; FILE REFERENCE: Case 20805
 ; CURRENT APPLICATION NUMBER: US/10/014,363
 ; CURRENT FILING DATE: 2001-12-11
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 169
 ; TYPE: PRT
 ; ORGANISM: CHO/dhfr-
 US-10-014-363-4

Query Match 95.8%; Score 856.5; DB 13; Length 169;
Best Local Similarity 97.1%; Pred. No. 5e-86; Indels 5; Gaps 1;
Matches 169; Conservative 0; Mismatches 0;

QY 1 APPRIEGRAPPLICDSRVLYLLEAKEAENITTCACCHCSLNENITVPDVKVNFYAKW 60
DB 1 APE-----APPLICDSRVLYLLEAKEAENITTCACCHCSLNENITVPDVKVNFYAKW 55
QY 61 RMEVGOQAVEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLSLTLRAL 120
DB 56 RMEVGOQAVEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLSLTLRAL 115
QY 121 GAKKEAISPPDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGDR 174
DB 116 GAKKEAISPPDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGDR 169

RESULT 5

US-10-435-608-8
; Sequence 8, Application US/10435608
; Publication No. US20030235536A1
; GENERAL INFORMATION:
; APPLICANT: Blumberg, Richard S.
; APPLICANT: Lencer, Wayne I.
; APPLICANT: Simister, Neil E.
; APPLICANT: Bitonti, Alan J.
; TITLE OF INVENTION: CENTRAL AIRWAY ADMINISTRATION FOR SYSTEMIC DELIVERY OF THERAPEUTIC
; FILE REFERENCE: S01383.70010.US
; CURRENT APPLICATION NUMBER: US/10/435, 608
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: PCT/US02/21335
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-435-608-8

Query Match 95.6%; Score 855; DB 14; Length 425;
Best Local Similarity 97.7%; Pred. No. 2.6e-85; Indels 3; Gaps 0;
Matches 167; Conservative 1; Mismatches 3;

QY 4 RIEGRAPPLICDSRVLYLLEAKEAENITTCACCHCSLNENITVPDVKVNFYAKWME 63
DB 20 RAGSRAPPLICDSRVLYLLEAKEAENITTCACCHCSLNENITVPDVKVNFYAKWME 79
QY 64 VGOQAVEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLSLTLRALGAQ 123
DB 80 VGOQAVEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLSLTLRALGAQ 139
QY 124 KEAISPPDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGDR 174
DB 140 KEAISPPDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGDR 190

RESULT 6

US-10-622-108-8
; Sequence 8, Application US/10622108
; Publication No. US20040063912A1
; GENERAL INFORMATION:
; APPLICANT: Blumberg, Richard S.
; APPLICANT: Lencer, Wayne I.
; APPLICANT: Simister, Neil E.
; APPLICANT: Bitonti, Alan J.
; TITLE OF INVENTION: CENTRAL AIRWAY ADMINISTRATION FOR SYSTEMIC DELIVERY OF THERAPEUTIC
; FILE REFERENCE: S01383.70011.US
; CURRENT APPLICATION NUMBER: US/10/622,108
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: US 10/435,608
; PRIOR FILING DATE: 2003-05-09

; PRIOR APPLICATION NUMBER: PCT/US02/21355
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/364,482
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-622-108-8

Query Match 95.6%; Score 855; DB 15; Length 425;
Best Local Similarity 97.7%; Pred. No. 2.6e-85; Indels 3; Gaps 0;
Matches 167; Conservative 1; Mismatches 3;

QY 4 RIEGRAPPLICDSRVLYLLEAKEAENITTCACCHCSLNENITVPDVKVNFYAKWME 63
DB 20 RAGSRAPPLICDSRVLYLLEAKEAENITTCACCHCSLNENITVPDVKVNFYAKWME 79
QY 64 VGOQAVEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLSLTLRALGAQ 123
DB 80 VGOQAVEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLSLTLRALGAQ 139
QY 124 KEAISPPDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGDR 174
DB 140 KEAISPPDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGDR 190

RESULT 7

US-09-853-731-2
; Sequence 2, Application US/09853731
; Patent No. US20020037841A1
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/09/853,731
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-731-2

Query Match 95.2%; Score 851; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85; Indels 0; Gaps 0;
Matches 166; Conservative 0; Mismatches 0;

QY 9 APPRICDSRVLYLLEAKEAENITTCACCHCSLNENITVPDVKVNFYAKWMEVGOQA 68
DB 1 APPRICDSRVLYLLEAKEAENITTCACCHCSLNENITVPDVKVNFYAKWMEVGOQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLSLTLRALGAOKEAIS 128
DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLSLTLRALGAOKEAIS 120
QY 129 PPDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGDR 174
DB 121 PPDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGDR 166

RESULT 8

US-10-014-363-2
; Sequence 2, Application US/10014363
; Publication No. US20020115833A1
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Engel, Alfred

```
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-363-2

Query Match          95.2%; Score 851; DB 13; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 68
Db 1 APRRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 129 PPDASAAPLRTITADTFRKLFRVYSNFLRGKLYTGACRTGDR 174
Db 121 PPDASAAPLRTITADTFRKLFRVYSNFLRGKLYTGACRTGDR 166

RESULT 9
US-10-241-356-2
; Sequence 2, Application US/10241356
; Publication No. US20030077753A1
; GENERAL INFORMATION:
; APPLICANT: TISCHER, WILHELM
; TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
; FILE REFERENCE: 20971
; CURRENT APPLICATION NUMBER: US/10/241,356
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: EP 01122555.4
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-241-356-2

Query Match          95.2%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 68
Db 1 APRRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 129 PPDASAAPLRTITADTFRKLFRVYSNFLRGKLYTGACRTGDR 174
Db 121 PPDASAAPLRTITADTFRKLFRVYSNFLRGKLYTGACRTGDR 166

RESULT 10
US-10-293-551-2
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```
; Sequence 2, Application US/10293551
; Publication No. US20030120045A1
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/10/293,551
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/09/604,938
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-551-2

Query Match          95.2%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 68
Db 1 APRRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 129 PPDASAAPLRTITADTFRKLFRVYSNFLRGKLYTGACRTGDR 174
Db 121 PPDASAAPLRTITADTFRKLFRVYSNFLRGKLYTGACRTGDR 166

RESULT 11
US-10-400-377-2
; Sequence 2, Application US/10400377
; Publication No. US20030162949A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,377
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-377-2

Query Match          95.2%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 68
Db 1 APRRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60
```

```

RESULT 13
US-10-298-148-2
; Sequence 2, Application US/10298148
; Publication No. US20030171284A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/298,148
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-148-2

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; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01174
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-467-115-1

Query Match      95.2%; Score 851; DB 15; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85; 0; Indels 0; Gaps 0;
Matches 166; Conservative 0; Mismatches 0;

QY      9 APPRLICDSRVLELYLLEAKEAENITTGCAEHCSLNENITVPTDKVNFYAWKRMEVGQQA 68
Db      1 APPRLICDSRVLELYLLEAKEAENITTGCAEHCSLNENITVPTDKVNFYAWKRMEVGQQA 60

QY      69 VEVWQGLALLSEAVLRGQALLVNSSQFWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 128
Db      61 VEVWQGLALLSEAVLRGQALLVNSSQFWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 120

QY      129 PPDAASAAPLRTITADTERKLFRVYSNFLRGKLYTGACRTGDR 174
Db      121 PPDAASAAPLRTITADTERKLFRVYSNFLRGKLYTGACRTGDR 166

Search completed: November 19, 2004, 21:32:13
Job time : 83.4565 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 20:59:24 ; Search time 20.1934 Seconds
(without alignments)
829.068 Million cell updates/sec

Title: US-10-014-363-3

Perfect score: 894

Sequence: 1 APPRIEGRAPPLICDSRVL.....NFLRGKLYTGACRTGDR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	95.2	193	1 ZUHU	erythropoietin pre
2	769.5	86.1	192	1 JQ0173	erythropoietin pre
3	764.5	85.5	192	1 I84613	erythropoietin pre
4	718	80.3	188	1 I46083	erythropoietin pre
5	706	79.0	192	1 S28148	erythropoietin pre
6	690.5	77.2	194	1 I46401	erythropoietin pre
7	686	76.7	192	1 A24902	erythropoietin pre
8	685.5	76.7	195	2 JC7699	erythropoietin pre
9	683	76.4	190	2 I46578	erythropoietin - r
10	638	71.4	175	2 I46199	erythropoietin - p
11	91.5	10.2	813	2 AF0526	erythropoietin - d
12	90	10.1	353	2 G02729	ATP-dependent heli
13	89	10.0	353	2 I80105	thrombopoietin - h
14	88	9.8	323	2 AB0323	thrombopoietin pre
15	87.5	9.8	346	2 AE0959	ribonucleoside-dip
16	87.5	9.8	824	2 D64738	Solute binding rec
17	86	9.6	286	2 A55330	ATP-dependent heli
18	85	9.5	339	2 A83274	megakaryocyte grow
19	83.5	9.3	296	2 AI0443	UDP-N-acetylpyruvo
20	82.5	9.2	824	2 H85498	probable 2-hydroxy
21	82.5	9.2	824	2 H90647	helicase, ATP-depe
22	81.5	9.1	3033	1 GNMVJ8	genome polyprotein
23	79.5	8.9	480	2 S56639	ribosomal protein
24	79.5	8.9	1829	2 T35681	probable sensory h
25	78.5	8.8	897	2 A54696	EGF receptor subst
26	78	8.7	348	2 T35450	ABC transporter Ar
27	78	8.7	455	2 H97693	conserved hypothet
28	78	8.7	455	2 H97693	methylamine utiliz
29	78	8.7	747	1 S36741	probable copper-tr

ALIGNMENTS

RESULT 1

ZUHU

erythropoietin precursor [validated] - human

C;Species: Homo sapiens (man)

C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004

C;Accession: A01855; A24744; A25384; A22210; S56178

R;Jacobs, K.; Shoemaker, C.; Rudersdorf, R.; Neill, S.D.; Kaufman, R.J.; Mufson, A.; See

Nature 313, 806-810, 1985

A;Title: Isolation and characterization of genomic and cDNA clones of human erythropoiet

A;Reference number: A01855; MUID:85137899; PMID:3838366

A;Accession: A01855

A;Molecule type: mRNA; DNA

A;Residues: 1-193 <JAC>

A;Cross-references: UNIPROT:P01588; GB:X02157; GB:X02158

Proc. Natl. Acad. Sci. U.S.A. 82, 7580-7584, 1985

A;Title: Cloning and expression of the human erythropoietin gene.

A;Reference number: A24744; MUID:86067948; PMID:3865178

A;Accession: A24744

A;Molecule type: DNA

A;Residues: 1-193 <LIN>

A;Cross-references: GB:M13319; NID:g182197; PIDN:AAAS2400.1; PID:g182198

R;Lai, P.H.; Everett, R.; Wang, F.F.; Arakawa, T.; Goldwasser, E.

J. Biol. Chem. 261, 3116-3121, 1986

A;Title: Structural characterization of human erythropoietin.

A;Reference number: A25384; MUID:86140080; PMID:3949763

A;Accession: A25384

A;Molecule type: protein

A;Residues: 28-86, 'Q', 87-193 <LAI>

A;Experimental source: urine

A;Note: Forms without the carboxyl-terminal residue and the four carboxyl-terminal resid

R;Yanagawa, S.; Hirade, K.; Ohnata, H.; Sasaki, R.; Chiba, H.; Ueda, M.; Goto, M.

J. Biol. Chem. 259, 2707-2710, 1984

A;Title: Isolation of human erythropoietin with monoclonal antibodies.

A;Reference number: A22210; MUID:84135751; PMID:6698989

A;Accession: A22210

A;Molecule type: protein

A;Residues: 28-29, 'X', 31-33, 'L', 35-50, 'X', 52-53, 'D', 55, 'G', 57 <YAN>

R;Matsumoto, S.; Ikura, K.; Ueda, M.; Sasaki, R.

Plant Mol. Biol. 27, 1163-1172, 1995

A;Title: Characterization of a human glycoprotein (erythropoietin) produced in cultured

A;Reference number: S56178; MUID:95284365; PMID:7766897

A;Accession: S56178

A;Molecule type: protein

A;Residues: 28-33, 'X', 35-37 <MTS>

C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o

C;Genetics:

A;Gene: GDB:EPO

A;Cross-references: GDB:119110; OMIM:133170

A;Map position: 7q21.3-7q22.1

A;Introns: 5/1; 53/3; 82/3; 142/3

C;Function:

A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status experimental
F;34-188,56-60/disulfide bonds: #status experimental
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;152/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 95.2%; Score 851; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 4.6e-73;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKFNFYAKRMEVQQA 68
DB 28 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKFNFYAKRMEVQQA 87

QY 69 VEVWQGLALLSEAVLRGQALLVNSOPWEPLOLHVVDKAVSGLRSLTTLRALGAQKEAIS 128
DB 88 VEVWQGLALLSEAVLRGQALLVNSOPWEPLOLHVVDKAVSGLRSLTTLRALGAQKEAIS 147

QY 129 PPDASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 174
DB 148 PPDASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 193

RESULT 2
JQ0173
erythropoietin precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 07-Sep-1990 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: JQ0173
R;Lin, F.K.; Lin, C.H.; Lai, P.H.; Browne, J.K.; Egrie, J.C.; Smalling, R.; Fox, G.M.; O
Gene 44, 201-209, 1986
A;Title: Monkey erythropoietin gene: cloning, expression and comparison with the human e
A;Reference number: JQ0173; MUID:87055236; PMID:2877922
A;Accession: JQ0173
A;Molecule type: mRNA
A;Residues: 1-192 <LIN>
A;Cross-references: UNIPROT:P07865; GB:M18189; GB:M15818; GB:M15819; GB:M18188; NID:9342
A;Experimental source: kidney
C;Comment: This protein is the principal hormone involved in the regulation of erythrocy
C;Function: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 86.1%; Score 769.5; DB 1; Length 192;
Best Local Similarity 91.6%; Pred. No. 2.3e-65;
Matches 152; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 9 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKFNFYAKRMEVQQA 68
DB 28 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKFNFYAKRMEVQQA 87

QY 69 VEVWQGLALLSEAVLRGQALLVNSOPWEPLOLHVVDKAVSGLRSLTTLRALGAQKEAIS 128
DB 88 VEVWQGLALLSEAVLRGQALLVNSOPWEPLOLHVVDKAVSGLRSLTTLRALGAQKEAIS 146

QY 129 PPDASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 174
DB 147 LPDASAAPLRTITADTFCKLFRVYSNFLRGKLYTGACRRGDR 192

RESULT 3
I84613
erythropoietin precursor - rhesus macaque

C;Species: Macaca mulatta (rhesus macaque)
C;Date: 02-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: I84613
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I84613
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-192 <RES>
A;Cross-references: UNIPROT:Q28513; GB:LI0609; NID:G342095; PIDN:AAA36842.1; PID:G342096
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function:
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 85.5%; Score 764.5; DB 1; Length 192;
Best Local Similarity 90.4%; Pred. No. 6.9e-65;
Matches 150; Conservative 9; Mismatches 6; Indels 1; Gaps 1;

QY 9 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKFNFYAKRMEVQQA 68
DB 28 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKFNFYAKRMEVQQA 87

QY 69 VEVWQGLALLSEAVLRGQALLVNSOPWEPLOLHVVDKAVSGLRSLTTLRALGAQKEAIS 128
DB 88 VEVWQGLALLSEAVLRGQALLVNSOPWEPLOLHVVDKAVSGLRSLTTLRALGAQKEAIS 146

QY 129 PPDASAAPLRTITADTFKFLFRVYSNFLRGKLYTGACRTGDR 174
DB 147 LPDASAAPLRTITADTFCKLFRVYSNFLRGKLYTGACRRGDR 192

RESULT 4
I46083
erythropoietin precursor - cat (fragment)
C;Species: Felis silvestris catus (domestic cat)
C;Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: I46083
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I46083
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-188 <WEN>
A;Cross-references: UNIPROT:P33708; GB:LI0606; NID:G163820; PIDN:AAA30807.1; PID:G163821
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function:
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-188/Product: erythropoietin #status predicted <MAT>
F;29-183,51-55/disulfide bonds: #status predicted
F;46,60,105/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 80.3%; Score 718; DB 1; Length 188;
Best Local Similarity 84.3%; Pred. No. 1.7e-60;
Matches 140; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKFNFYAKRMEVQQA 68
DB 23 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKFNFYAKRMEVQQA 82

A;Residues: 1-194 <FUX>
A;Cross-references: UNIPROT:P33709; EMBL:Z24681; NID:G395049; PIDN:CAA80848.1; PID:G395049
R;Wen, D.; Boiesel, J.
Bio 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homology
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I47077
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 4-15, '1', 17-107, 'P', 109-194 <WEN>
A;Cross-references: GB:L10610; NID:G165876; PIDN:AAA31518.1; PID:G165877
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of C;Function:
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;24-189/Product: erythropoietin #status predicted <MAT>
F;34-184,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carboxydrate (Asn) (covalent) #status predicted
F;154/Binding site: carboxydrate (Ser) (covalent) #status predicted

Query Match 77.2%; Score 690.5; DB 1; Length 194;
Best Local Similarity 82.0%; Pred. No. 6.9e-58;
Matches 137; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

Qy 9 APPRLCDSRVLYRLLLEAKEAENITTCAGHCSLNNENITVPDTKVNIFYAKRMVEVQQA 68
Db APPRLCDSRVLYRLLLEAKEAENITTCAGHCSLNNENITVPDTKVNIFYAKRMVEVQQA 87
Qy 69 VEVWQGLALLSAVLRGQALLVNSQWPEPLQHLVDKAVSGLRSLTLTLRALGAKQKSAIS 128
Db LEVWQGLALLSAVLRGQALLVNSQWPEPLQHLVDKAVSGLRSLTLTLRALGAKQKSAIP 147
Qy 129 PPDAASAPLRTITADTPKFLPRVYSNFRGLKLYTGEACRTGDR 174
Db LPDATPSAAPLRITFTVDALSKPRIYSNFRGLKLYTGEACRRGDR 194

RESULT 7
A24902
erythropoietin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Oct-1987 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: A24902; A24901
R;Shoemaker, C.B.; Mitsock, L.D.
Mol. Cell. Biol. 6, 849-858, 1986
A;Title: Murine erythropoietin gene: cloning, expression, and human gene homology.
A;Reference number: A24902; MUID:87039105; PMID:3773894
A;Accession: A24902
A;Molecule type: DNA
A;Residues: 1-192 <SHO>
A;Cross-references: UNIPROT:P07321
A;Note: the authors translated the codon TTA for residue 12 as Phe, TTA for residue 43 as E.
R;McDonald, J.D.; Lin, F.K.; Goldwasser, E.
Mol. Cell. Biol. 6, 842-848, 1986
A;Title: Cloning, sequencing, and evolutionary analysis of the mouse erythropoietin gene
A;Reference number: A24901; MUID:87039104; PMID:3022133
A;Accession: A24901
A;Molecule type: DNA
A;Residues: 1-67, 'P', 69-192 <MCD>
A;Cross-references: GB:M12930; NID:G193086; PIDN:AAA37570.1; PID:G387152
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of C;Genetics:
A;Introns: 5/1; 52/3; 81/3; 141/3
C;Function:
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-132/Product: erythropoietin #status predicted <MAT>
F;33-187,55-165/Disulfide bonds: #status predicted
F;50,64,109/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 76.7%; Score 686; DB 1; Length 192;
 Best Local Similarity 79.5%; Pred. No. 1.8e-57;
 Matches 132; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGOQA 68
 DB 27 APPRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGOQA 86

QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVVDKAVSGRLSLTLLRALGAQKEAIS 128
 DB 87 IEVWQGLSLLSAILQQAALLANSQPPETLQHLIDKALSGRLSLTLLRALGAQKEAIS 146

QY 129 PPDAAAPLRITITADTFKLFPRVYSNFRGKLYTGACRTGDR 174
 DB 147 PPDTPPPAPLRITITADTFKLFPRVYSNFRGKLYTGACRTGDR 192

RESULT 8
 JC7699
 erythropoietin - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
 C:Accession: JC7699
 R:Vilalta, A.; Wu, D.; Margalith, M.; Hobart, P.
 Biochem. Biophys. Res. Commun. 284, 823-827, 2001
 A:Title: Rabbit EPO gene and cDNA: Expression of rabbit EPO after intramuscular injection
 A:Reference number: JC7699; MUID:21290682; PMID:11396976
 A:Contents: Kidney
 A:Accession: JC7699
 A:Molecule type: DNA
 A:Residues: 1-195 <VIL>
 A:Cross-references: GB:AF290943
 C:Comment: This protein, a heavily glycosylated 34K protein produced in the fetal liver
 cytes.
 C:Genetics:
 A:Gene: epo
 C:Superfamily: erythropoietin
 C:Keywords: glycoprotein; kidney

Query Match 76.4%; Score 685.5; DB 2; Length 195;
 Best Local Similarity 81.4%; Pred. No. 2.1e-57;
 Matches 136; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 9 APPRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGOQA 68
 DB 29 APARLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGOQA 88

QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVVDKAVSGRLSLTLLRALGAQKEAIS 128
 DB 89 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVVDKAVSGRLSLTLLRALGAQKEAIS 148

QY 129 PPDAAAPLRITITADTFKLFPRVYSNFRGKLYTGACRTGDR 174
 DB 149 PPDAAAPLRITITADTFKLFPRVYSNFRGKLYTGACRTGDR 195

RESULT 9
 I46578
 erythropoietin - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C:Accession: I46578
 R:Wen, D.; Boissel, J.
 Blood 82, 1507-1516, 1993
 A:Title: Erythropoietin structure-function relationships: High degree of sequence homology
 A:Reference number: I46083; MUID:93372347; PMID:8364201
 A:Accession: I46578
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-190 <WEN>
 A:Cross-references: UNIPROT:P49157; GB:I10607; NID:g164445; PIDN:AAA31029.1; PID:g164446
 C:Superfamily: erythropoietin

Query Match 76.4%; Score 683; DB 2; Length 190;
 Best Local Similarity 82.1%; Pred. No. 3.4e-57;
 Matches 138; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

QY 9 APPRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGOQA 68
 DB 23 APPRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGOQA 82

QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVVDKAVSGRLSLTLLRALGAQKEAIS 128
 DB 83 MEVWQGLALLSAILQQAALLANSQPPSEALQHVVDKAVSGRLSLTLLRALGAQKEAIS 142

QY 129 PPDAAAPLRITITADTFKLFPRVYSNFRGKLYTGACRTGDR 174
 DB 143 LPDASFPSSATPLRTFAVDTLCKLFRVYSNFRGKLYTGACRTGDR 190

RESULT 10
 I46199
 erythropoietin - dog (fragment)
 C:Species: Canis lupus familiaris (dog)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C:Accession: I46199
 R:Wen, D.; Boissel, J.
 Blood 82, 1507-1516, 1993
 A:Title: Erythropoietin structure-function relationships: High degree of sequence homology
 A:Reference number: I46083; MUID:93372347; PMID:8364201
 A:Accession: I46199
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-175 <WEN>
 A:Cross-references: UNIPROT:P33707; GB:I13027; NID:g290087; PIDN:AAA30842.1; PID:g552347
 C:Superfamily: erythropoietin

Query Match 71.4%; Score 638; DB 2; Length 175;
 Best Local Similarity 81.0%; Pred. No. 5.6e-53;
 Matches 124; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGOQA 68
 DB 23 APPRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGOQA 82

QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVVDKAVSGRLSLTLLRALGAQKEAIS 128
 DB 83 LEVWQGLALLSEAVLRGQALLVNSQWPPELQHVVDKAVSGRLSLTLLRALGAQKEAIS 142

QY 129 PPDAAAPLRITITADTFKLFPRVYSNFRGKLYTGACRTGDR 161
 DB 143 LPDASFPAPLRITITADTFKLFPRVYSNFRGKLYTGACRTGDR 175

RESULT 11
 AF0526
 ATP-dependent helicase HrpB [imported] - Salmonella enterica subsp. enterica serovar Typhi
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 12-Jun-2003
 C:Accession: AF0526
 R:Parkhill, J.; Dougan, K.D.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Moule, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whittam, T.S.; Farrar, J.; Dougan, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Moule, S.; O'Garra, P.
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AF0526
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-813 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD01350.1; PID:g16501478; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY0214

C;Superfamily: ATP-dependent RNA helicase, HrpB type

Query Match 10.2%; Score 91.5; DB 2; Length 813;
Best Local Similarity 27.1%; Pred. No. 1.7;
Matches 45; Conservative 20; Mismatches 46; Indels 55; Gaps 9;
QY 1 APPRIEGRAPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVNFAWK 60
Db 538 APLLQGSASP---DARIL---LAQPLDIASLIQACPDLLRQSDIVDEWDEAGTILKAWR 590
QY 61 RMEVGGQAEVWQGLALLSEAVRGQALLVN-----SSQWEP-----LQJH----- 102
Db 591 RMRIGQLTVSV-QPLAKPSEELH-QAMLINGIRDKGLSVLWTPPEAQFRLRLHCAAKWL 648
QY 103 -----VDKA-----VSLRLSITTL-----LRAL 120
Db 649 PEYDWPVAVDEASLLATLENWLLPHMTGVQSLRLSLKSLNVTQALRGL 694

RESULT 12

G02729
thrombopoietin - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C;Accession: G02729

submitted to the EMBL Data Library, May 1996

A;Reference number: H01637
A;Accession: G02729
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-353 <IMX>
A;Cross-references: EMBL:U59493; NID:g1401245; PIDN:AAB03392.1; PID:g1401246
C;Genetics:
A;Gene: HPO

Query Match 10.1%; Score 90; DB 2; Length 353;
Best Local Similarity 26.3%; Pred. No. 0.87;
Matches 41; Conservative 20; Mismatches 75; Indels 20; Gaps 5;

QY 9 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVNFAWKMEVGGQA 68
Db 24 APP--ACDLRLVLSKLLRDSHVLSKLSQCPEVHPPLTPVLLPAVDPSLGWKMTQMBETKA 81
QY 69 VEVWQGLALLSEAVL--RQALLVNSQPEWPEPLQLHVDKAVSGLRSLTLLRALGAQKEA 126
Db 82 QDILGAVTLLLEGVWAARGQLGPTCLSSLLGQSEQVRLLLGALQSL-----LGTQ--- 132
QY 127 ISPPDAASAAPRLTITADTFKRLFRVYNSFLRGKXK 162
Db 133 -LPPQG-----RTTAHKDPNAIFLSFQHLRGKVR 161

RESULT 13

I80105
thrombopoietin precursor - human
N;Alternate names: c-MPL ligand; megakaryocyte growth and development factor precursor
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: I59281; I80105; S45331; S48740; I38672; I52610
R;Poster, D.C.; Sprecher, C.A.; Grant, F.J.; Kramer, J.M.; Kuijper, J.L.; Holly, R.D.; W
Proc. Natl. Acad. Sci. U.S.A. 91, 13023-13027, 1994
A;Title: Human thrombopoietin: gene structure, cDNA sequence, expression, and chromosoma
A;Reference number: I59281; MUID:95108091; PMID:7809166
A;Accession: I59281
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-353 <RE2>

A;Cross-references: UNIPROT:P40225; GB:I36051; NID:g533214; PIDN:AAC37568.1; PID:g533215
A;Accession: I80105
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-353 <RES>

A;Cross-references: GB:I36052; NID:g533216; PIDN:AAC37566.1; PID:g533217
R;de Sauvage, F.J.; Haas, P.E.; Spencer, S.D.; Malloy, B.E.; Gurney, A.L.; Spencer, S.A.
D.V.; Eaton, D.L.
Nature 369, 533-538, 1994
A;Title: Stimulation of megakaryocytopoiesis and thrombopoiesis by the c-Mpl ligand.
A;Reference number: S45331; MUID:94261202; PMID:8202154
A;Accession: S45331
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-353 <SAU>
A;Cross-references: GB:I33410; NID:g506826; PIDN:AAA59857.1; PID:g506827
R;Sohma, Y.; Akahori, H.; Seki, N.; Hori, T.; Ogami, K.; Kato, T.; Shimada, Y.; Kawamura
FEBS Lett. 353, 57-61, 1994
A;Title: Molecular cloning and chromosomal localization of the human thrombopoietin gene
A;Reference number: S48740; MUID:95010765; PMID:7926023
A;Accession: S48740
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-353 <SOH>
A;Cross-references: GB:D32046; NID:g577319; PIDN:BAA06807.1; PID:g577320
R;Bartley, T.D.; Bogenberger, J.; Hunt, P.; Li, Y.S.; Lu, H.S.; Martin, F.; Chang, M.S.;
Cell 77, 1117-1124, 1994
A;Title: Identification and cloning of a megakaryocyte growth and development factor tha
A;Reference number: A54463; MUID:94291201; PMID:8020099
A;Accession: I38672
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112, 'E', 114-353 <RE3>
A;Cross-references: EMBL:U11025; NID:g511223; PIDN:AAA50553.1; PID:g558078
R;Gurney, A.L.; Kuang, W.J.; Xie, M.H.; Malloy, B.E.; Eaton, D.L.; de Sauvage, F.J.
Blood 85, 981-988, 1995
A;Title: Genomic structure, chromosomal localization, and conserved alternative splice f
A;Reference number: I52610; MUID:95152076; PMID:7849319
A;Accession: I52610
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-353 <RE4>
A;Cross-references: GB:S76771; NID:g914225; PIDN:AAB33390.1; PID:g914226
C;Genetics:
A;Gene: GDB:THPO; MGDF
A;Cross-references: GDB:374007; OMIM:600044
A;Map position: 3q26.3-3q27
A;Introns: 5/1; 47/3; 76/3; 132/3
C;Keywords: alternative splicing; cytokine; glycoprotein

Query Match 10.0%; Score 89; DB 2; Length 353;
Best Local Similarity 26.3%; Pred. No. 1.1;
Matches 41; Conservative 20; Mismatches 75; Indels 20; Gaps 5;

QY 9 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVNFAWKMEVGGQA 68
Db 24 APP--ACDLRLVLSKLLRDSHVLSKLSQCPEVHPPLTPVLLPAVDPSLGWKMTQMBETKA 81
QY 69 VEVWQGLALLSEAVL--RQALLVNSQPEWPEPLQLHVDKAVSGLRSLTLLRALGAQKEA 126
Db 82 QDILGAVTLLLEGVWAARGQLGPTCLSSLLGQSEQVRLLLGALQSL-----LGTQ--- 132
QY 127 ISPPDAASAAPRLTITADTFKRLFRVYNSFLRGKXK 162
Db 133 -LPPQG-----RTTAHKDPNAIFLSFQHLRGKVR 161

RESULT 14

AB0323
ribonucleoside-diphosphate reductase (EC 1.17.4.1) beta chain [imported] - Versinia pestis
C;Species: Versinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0323
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Versinia pestis, the causative agent of plague.

Search completed: November 19, 2004, 21:12:04
Job time : 22.1934 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 20:59:03 ; Search time 103.996 Seconds
(without alignments)
962.682 Million cell updates/sec

Title: US-10-014-363-3

Perfect score: 894

Sequence: 1 APPRIEGRAPPLICDSRVL.....NFLRGKLYTGEACRTGDR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	851	95.2	193	1	EPO HUMAN	P01588 homo sapien
2	851	95.2	193	2	AAP22357	Aap22357 homo sapi
3	769.5	86.1	192	1	EPO MACFA	P07865 macaca fasc
4	764.5	85.5	192	1	EPO MACMU	Q28513 macaca mula
5	728	81.4	192	2	Q86781	Q86781 equus cabal
6	711	79.5	192	1	EPO FELCA	P33708 felis silve
7	706	79.0	192	1	EPO RAT	P29676 rattus norv
8	698	78.1	206	2	O6PWU5	O6pwu5 canis fami
9	698	78.1	206	2	AAS77874	Aas77874 canis fam
10	697.5	78.0	192	1	EPO BOVIN	P48617 bos taurus
11	694	77.6	192	1	EPO MOUSE	P07321 mus musculu
12	690.5	77.2	194	1	EPO SHEEP	P33709 ovis aries
13	685.5	76.7	195	2	O9GKA2	O9gka2 cryptolagus
14	685.5	76.7	195	2	O9GKA3	O9gka3 oryctolagus
15	683	76.4	190	1	EPO PIG	P49157 sus scrofa
16	683	76.4	192	2	Q6H8S9	Q6h8s9 spalax juda
17	683	76.4	192	2	Q6H8T0	Q6h8t0 spalax juda
18	683	76.4	192	2	Q6H8T1	Q6h8t1 spalax carm
19	683	76.4	194	2	Q9MYM8	Q9mym8 sus scrofa
20	679	76.0	192	2	Q6H8T2	Q6h8t2 spalax gola
21	663	74.2	133	2	Q8H288	Q8h288 gorilla gor
22	658	73.6	133	2	Q8H289	Q8h289 pan troglod
23	638	70.1	175	1	EPO CANFA	P33707 canis fami
24	627	70.1	131	2	Q8H287	Q8h287 pongo pygma
25	607	67.9	133	2	Q8H286	Q8h286 macaca sp.
26	554	62.0	133	2	Q8H285	Q8h285 saguinus oe
27	241	27.0	195	2	Q6UAMI	Q6uami tetraodon n
28	241	27.0	195	2	AAR25698	Aar25698 tetraodon
29	238	26.6	182	2	Q6JV23	Q6jv23 fugu rubrip
30	238	26.6	182	2	AAQ72466	Aaq72466 fugu rubr
31	238	26.6	185	2	Q6JV22	Q6jv22 fugu rubrip

RESULT 1

ID	EPO HUMAN	STANDARD;	PRT;	193 AA.
AC	P01588; Q9UDZ0; Q9UEZ5; Q9UHA0;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Erythropoietin precursor (Epoetin).			
GN	Name=EPO;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85137899; PubMed=3838366;			
RA	Jacobs K., Shoemaker C., Ruderstorf R., Neill S.D., Kaufman R.J.,			
RA	Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F.,			
RA	Kawakita M., Shimizu T., Miyake T.,			
RT	"Isolation and characterization of genomic and cDNA clones of human			
RT	erythropoietin.";			
RL	Nature 313:806-810(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86067948; PubMed=3865178;			
RA	Lin F.-K., Suggs S., Lin C.-H., Browne J.K., Smalling R., Egrie J.C.,			
RA	Chen K.K., Fox G.N., Martin F., Stabinsky Z., Badrawi S.M., Lai P.-H.,			
RA	Goldwasser E.;			
RT	"Cloning and expression of the human erythropoietin gene.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99018118; PubMed=9799793;			
RA	Gloekner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,			
RA	Tsui L.-C., Rosenthal A.;			
RT	"Large-scale sequencing of two regions in human chromosome 7q22:			
RT	analysis of 650 kb of genomic sequence around the EPO and CUGL1 loci			
RT	reveals 17 genes.";			
RL	Genome Res. 8:1060-1073(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	Rupert J.L., Hochacka P.W.;			
RA	"Erythropoietin gene sequence in the Quechua, a high altitude native			
RT	population.";			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 58-193 FROM N.A., AND VARIANTS HEPATOCELLULAR CARCINOMA			
RP	131-ASN-PHE-132 AND GLN-149.			
RX	MEDLINE=93384593; PubMed=8396923;			
RA	Funakoshi A., Muta H., Baba T., Shimizu S.;			
RT	"Gene expression of mutant erythropoietin in hepatocellular			
RT	carcinoma.";			
RL	Biochem. Biophys. Res. Commun. 195:717-722(1993).			
RN	[6]			

Aaq72467 fugu rubr
Q9qv40 rattus sp.
Q6iye9 gallus gall
P42705 canis fami
Q829b9 salmonella
P40225 homo sapien
Q8zdc8 yersinia pe
Aas62651 yersinia
Q8z2m5 salmonella
Q8zkz4 salmonella
Q7qdz2 anopheles g
Q7zdk7 brachydanio
P37024 escherichia
Q8zrq4 salmonella

ALIGNMENTS

32	238	26.6	185	2	AAQ72467
33	188	21.0	50	2	Q9QV40
34	118.5	13.3	177	2	Q6IYE9
35	109	12.2	352	1	TPO CANFA
36	91.5	10.2	813	2	Q829B9
37	89	10.0	353	1	TPO HUMAN
38	88	9.8	323	2	Q8ZDC8
39	88	9.8	323	2	AAS62651
40	87.5	9.8	346	2	Q8Z2M5
41	87.5	9.8	346	2	Q8ZKZ4
42	87.5	9.8	432	2	Q7QDZ2
43	87.5	9.8	558	2	Q7ZDK7
44	87.5	9.8	809	1	HRPB ECOLI
45	87.5	9.8	824	2	Q8ZRQ4

SEQUENCE OF 28-193, AND DISULFIDE BONDS.
TISSUE=urine;
MEDLINE=86140080; PubMed=3949763;
Lai P.H., Everett R., Wang F.F., Arakawa T., Goldwasser E.;
"Structural characterization of human erythropoietin.";
J. Biol. Chem. 261:3116-3121(1986).
[7]
PRELIMINARY SEQUENCE OF 28-57.
MEDLINE=84135751; PubMed=6698989;
Yanagawa S., Hirade K., Ohnata H., Sasaki R., Chiba H., Ueda M.,
Goto M.;
"Isolation of human erythropoietin with monoclonal antibodies.";
J. Biol. Chem. 259:2707-2710(1984).
[8]
STRUCTURE OF CARBOHYDRATES.
MEDLINE=88153657; PubMed=3346214;
Takeuchi M., Takasaki S., Miyazaki H., Kato T., Hoshi S., Kochibe N.,
Kobata A.;
"Comparative study of the asparagine-linked sugar chains of human
erythropoietins purified from urine and the culture medium of
recombinant Chinese hamster ovary cells.";
J. Biol. Chem. 263:3657-3663(1988).
[9]
STRUCTURE OF CARBOHYDRATES.
MEDLINE=89118279; PubMed=3219367;
Sasaki H., Ochi N., Dell A., Fukuda M.;
"Site-specific glycosylation of human recombinant erythropoietin:
analysis of glycopeptides or peptides at each glycosylation site by
fast atom bombardment mass spectrometry.";
Biochemistry 27:8618-8626(1988).
[10]
STRUCTURE OF CARBOHYDRATES.
MEDLINE=92314463; PubMed=1820196;
Takeuchi M., Kobata A.;
"Structures and functional roles of the sugar chains of human
erythropoietins.";
Glycobiology 1:337-346(1991).
[11]
X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE=98445092; PubMed=9774108; DOI=10.1038/26773;
Syed R.S., Reid S.W., Li C., Cheetham J.C., Aoki K.H., Liu B.,
Zhang H., Oslund T.D., Chirino A.J., Zhang J., Finer-Moore J.,
Elliot S., Siney K., Katz B.A., Matthews D.J., Wendoloski J.J.,
Egrie J., Stroud R.M.;
"Efficiency of signalling through cytokine receptors depends
critically on receptor orientation.";
Nature 395:511-516(1998).
-!- FUNCTION: Erythropoietin is the principal hormone involved in the
regulation of erythrocyte differentiation and the maintenance of a
physiological level of circulating erythrocyte mass.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
and by liver of fetal or neonatal mammals.
-!- PHARMACEUTICAL: Used for the treatment of anemia. Available under
the names Epogen (Amgen), Epogin (Chugai), Epomax (Elanex), Eprex
(Janssen-Cilag), Neorecormon or Recormon (Roche), and Procrit
(Ortho Biotech). Variations in the glycosylation pattern of EPO
distinguishes these products. Epogen, Epogin, Eprex and Procrit
are generically known as epoetin alfa, Neorecormon and Recormon as
epoetin beta and Epomax as epoetin omega.
-!- SIMILARITY: Belongs to the EPO / TPO family.
-!- DATABASE: NAME-RED Systems' cytokine source book; EPO;
WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=197".

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EMBL; X02158; CAA26095.1; --

DR EMBL; X02157; CAA26094.1; --
DR EMBL; M11319; AA352400.1; --
DR EMBL; AF053356; AAC78791.1; --
DR EMBL; AF202308; AAF23132.1; --
DR EMBL; AF202306; AAF23132.1; JOINED.
DR EMBL; AF202307; AAF23132.1; JOINED.
DR EMBL; AF202310; AAF23133.1; --
DR EMBL; AF202309; AAF23133.1; JOINED.
DR EMBL; AF202311; AAF17572.1; --
DR EMBL; AF202314; AAF23134.1; --
DR EMBL; AF202312; AAF23134.1; JOINED.
DR EMBL; AF202313; AAF23134.1; JOINED.
DR EMBL; S65458; AAD13964.1; --
DR PIR; A01855; ZUHU.
DR PDB; 1B0Y; NMR; A=28-193.
DR PDB; 1CN4; X-ray; C=28-193.
DR PDB; 1EER; X-ray; A=28-193.
DR GlycoSuiteDB; P01588; --
DR Genew; HGNC:3415; EPO.
DR MIM; 133170; --
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0006950; P:response to stress; TAS.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR001323; EPO TPO.
DR InterPro; IPR003013; Erythroptn.
DR Pfam; PF00758; EPO TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO TPO; 1.
DR 3D-structure; Direct protein sequencing; Erythrocyte maturation;
KW Glycoprotein; Hormone; Pharmaceutical; Polymorphism; Signal.
FT SIGNAL 1 27 Erythropoietin.
FT CHAIN 28 193 Removed in mature form (Probable).
FT PROPEP 190 193
FT DISULFID 34 188
FT DISULFID 56 60
FT CARBOHYD 51 51 N-linked (GlcNAc...).
FT CARBOHYD 65 65 /FTId=CAR_000052.
FT CARBOHYD 110 110 N-linked (GlcNAc...).
FT CARBOHYD 153 153 /FTId=CAR_000166.
FT CARBOHYD 153 153 N-linked (GlcNAc...).
FT VARIANT 131 132 O-linked (GalNAc...).
FT SL -> NF (in an hepatocellular
carcinoma).
FT /FTId=VAR_009870.
FT P -> Q (in an hepatocellular carcinoma).
FT /FTId=VAR_009871.
FT E -> Q (in Ref. 1; CAA26095).
FT Q -> Q (in Ref. 5).
FT G -> R (in Ref. 1; CAA26095).
FT VARIANT 149 149
FT CONFLICT 40 40
FT CONFLICT 85 85
FT CONFLICT 140 140
FT HELIX 32 34
FT HELIX 36 52
FT HELIX 53 55
FT TURN 57 58
FT STRAND 61 68
FT STRAND 73 73
FT HELIX 75 78
FT TURN 79 80
FT HELIX 83 109
FT HELIX 118 138
FT TURN 139 140
FT HELIX 141 147
FT TURN 148 149
FT STRAND 160 164
FT HELIX 165 177
FT TURN 178 178
FT HELIX 179 188
FT SEQUENCE 193 AA; 21306 MW; C91F0E4C26A52033 CRC64;
SQ
Query Match 95.2%; Score 851; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.4e-71;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYLLEAKAEENITTCAGHCSLNENITVPDTKKNFYAKRMEVGQQA 68
 |||||
 Db 28 APRRLICDSRVLYLLEAKAEENITTCAGHCSLNENITVPDTKKNFYAKRMEVGQQA 87
 |||||
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 128
 |||||
 Db 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 147
 |||||
 QY 129 PPDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGDR 174
 |||||
 Db 148 PPDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGDR 193
 |||||

RESULT 2

AAP22357 PRELIMINARY; PRT; 193 AA.
 AC AAP22357;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein EPO.
 GN EPO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99063792; PubMed=9847074;
 RA Wilson R.;
 RT "Toward a complete human genome sequence."
 RL Genome Res. 8:1097-1108(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Doeber A., Elliott G., Jones T., Nguyen C., Stoneking T., Sun H.;
 RT "The sequence of Homo sapiens BAC clone RP11-336D7."
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.H.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC009488; AAP22357.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 193 AA; 21307 MW; C91F0E4C26A52033 CRC64;
 Query Match 95.2%; Score 851; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1.4e-71;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYLLEAKAEENITTCAGHCSLNENITVPDTKKNFYAKRMEVGQQA 68
 |||||
 Db 28 APRRLICDSRVLYLLEAKAEENITTCAGHCSLNENITVPDTKKNFYAKRMEVGQQA 87
 |||||
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 128
 |||||
 Db 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 147
 |||||
 QY 129 PPDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGDR 174
 |||||
 Db 148 PPDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGDR 193
 |||||

RESULT 3

EPO_MACFA

ID AC EPO_MACFA STANDARD; PRT; 192 AA.
 DT P07865;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=EPO;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87055236; PubMed=2877922;
 RA Lin F.-K., Lin C.-H., Lai P.-H., Browne J.K., Egrie J.C., Smalling R.,
 RA Fox G.M., Chen K.K., Castro M., Suggs S.;
 RT "Monkey erythropoietin gene: cloning, expression and comparison with
 the human erythropoietin gene."
 RL Gene 44:201-209(1986).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 regulation of erythrocyte differentiation and the maintenance of a
 physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
 CC
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 or send an email to license@sib-sib.ch).
 CC
 CC EMBL; M18189; AAA36841.1; -.
 DR PIR; JQ0173; JQ0173.
 DR HSSP; P01588; 1CN4.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR001323; EPO TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 27 By similarity.
 FT CHAIN 28 192 Erythropoietin.
 FT DISULFID 34 187 By similarity.
 FT DISULFID 56 60 By similarity.
 FT CARBOHYD 51 51 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 65 65 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 152 152 O-linked (GalNAc...) (By similarity).
 SQ SEQUENCE 192 AA; 21113 MW; E8A900F42AD4522 CRC64;
 Query Match 86.1%; Score 769.5; DB 1; Length 192;
 Best Local Similarity 91.6%; Pred. No. 6.1e-64;
 Matches 152; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 9 APRRLICDSRVLYLLEAKAEENITTCAGHCSLNENITVPDTKKNFYAKRMEVGQQA 68
 |||||
 Db 28 APRRLICDSRVLYLLEAKAEENITTCAGHCSLNENITVPDTKKNFYAKRMEVGQQA 87
 |||||
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 128
 |||||
 Db 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 146
 |||||
 QY 129 PPDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGDR 174
 |||||
 Db 147 PPDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGDR 192
 |||||

RESULT 4
 ID EPO MACMU STANDARD; PRT; 192 AA.
 AC Q28513;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=EPO;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Bolesel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 RA Czelusniak J., Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 RT sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 CC regulation of erythrocyte differentiation and the maintenance of a
 CC physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 CC and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; LI0609; AAA36842.1; -.
 DR PIR; I84613; I84613.
 DR HSSP; P01588; 1CN4.
 DR InterPro; IPR009079; 4 helix_cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 27 By similarity.
 FT CHAIN 28 192 Erythropoietin.
 FT DISULFID 34 187 By similarity.
 FT DISULFID 56 60 By similarity.
 FT CARBOHYD 51 51 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 65 65 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 152 152 O-linked (GalNAc...) (By similarity).
 SQ SEQUENCE 192 AA; 21081 MW; 275560A264628CD1 CRC64;
 Query Match 85.5%; Score 764.5; DB 1; Length 192;
 Best Local Similarity 90.4%; Pred. No. 1.8e-63;
 Matches 150; Conservative 9; Mismatches 6; Indels 1; Gaps 1;
 QY 9 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAKMEVQQA 68
 DB 28 APRLVCDSRVLYRLLEAKEAENITVTCGSSCSLNENITVPDTKNFYAKMEVQQA 87
 QY 69 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 128
 DB 88 VEVWQGLALLSEAVLRQAVLANSQPFEPLQLHMDKAIISGLRSITLLRALGAQ-BAIS 146

QY 129 PPDAASAAPLRTITADTPKFLRVYSNFRGLKLYTGEACRTGDR 174
 DB 147 LPDAASAAPLRTITADTFCKLFRVYSNFRGLKLYTGEACRGRDR 192
 RESULT 5
 Q867B1 PRELIMINARY; PRT; 192 AA.
 ID Q867B1;
 AC Q867B1;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Erythropoietin.
 GN Name=EPO;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX PubMed=14719696;
 RA Sato F., Yamashita S., Kugo T., Hasegawa T., Mitsui I.,
 RA Kijima-Suda I.;
 RT "Nucleotide sequence of equine erythropoietin and characterization of
 RT region-specific antibodies";
 RL Am. J. Vet. Res. 65:15-19(2004).
 DR EMBL; AB100030; BAC55239.1; -.
 DR HSSP; P01588; 1BUV.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 SQ SEQUENCE 192 AA; 20984 MW; E02D098490B09C4F CRC64;
 Query Match 81.4%; Score 728; DB 2; Length 192;
 Best Local Similarity 84.9%; Pred. No. 4.7e-60;
 Matches 141; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
 QY 9 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAKMEVQQA 68
 DB 27 APPRLICDSRVLYRLLEAKEAENITVTCGAGCSFGENVTPDTKNFYAKMEVQQA 86
 QY 69 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 128
 DB 87 VEVWQGLALLSEAVLRQALLVNSQPSETLRHVDKAVSSLSRLTLLRALGAQKEAIS 146
 QY 129 PPDAASAAPLRTITADTPKFLRVYSNFRGLKLYTGEACRTGDR 174
 DB 147 PPDAASAAPLRTFAVDTLCKLFRVYSNFRGLKLYTGEACRGRDR 192
 RESULT 6
 EPO_FELCA STANDARD; PRT; 192 AA.
 ID EPO_FELCA
 AC P33708;
 DT 01-PBB-1994 (Rel. 28, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=EPO;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.

Matches 139; Conservative 8; Mismatches 19; Indels 1; Gaps 1;

QY 9 APRILICDSRVLYLEAEKAEENITTCGAHCSLNENITVPTKYNFYAKRMEYQQA 68
 DB 26 APRILICDSRVLYLEAEKAEENITTCGAHCSLNENITVPTKYNFYAKRMEYQQA 85
 QY 69 VEVWQGLALLSEAVLQGALLVNSQWPEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 128
 DB 86 LEVWQGLALLSEAVLQGALLVNSQWPEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 145
 QY 129 PDAA-SAAPLRTITADTFRKLVNFRVSNFLRGKLYTGACRTGDR 174
 DB 146 LPDAPSAAPLRTITADTFRKLVNFRVSNFLRGKLYTGACRTGDR 192

RESULT 11
 EPO MOUSE
 ID EPO MOUSE STANDARD; PRT; 192 AA.
 AC P07321;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=Epo;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87039105; PubMed=3773894;
 RA Shoemaker C.B., Mitsock L.D.;
 RT "Murine erythropoietin gene: cloning, expression, and human gene
 RT homology";
 RL Mol. Cell. Biol. 6:849-858 (1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87039104; PubMed=3022133;
 RA McDonald J.D., Lin F.-K., Goldwasser E.;
 RT "Cloning, sequencing, and evolutionary analysis of the mouse
 RT erythropoietin gene";
 RL Mol. Cell. Biol. 6:842-848 (1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=129/Sv;
 RA MEDLINE=21138439; PubMed=11239002;
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
 RA Miller W., Koop B.F.;
 RT "Comparative analysis of the gene-dense ACHE/TFP2 region on human
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5";
 RL Nucleic Acids Res. 29:1352-1365 (2001).
 RN [4]
 RP SEQUENCE OF 1-52 FROM N.A.
 RX STRAIN=ICFW;
 RA MEDLINE=98030528; PubMed=9365246;
 RA Chretien S., Duprez V., Maouche L., Gisselbrecht S., Mayeux P.,
 RA Lacombe C.;
 RT "Abnormal erythropoietin (Epo) gene expression in the murine
 RT erythroleukemia IM32 cells results from a rearrangement between the G-
 RT protein beta2 subunit gene and the Epo gene";
 RL Oncogene 15:1995-1999 (1997).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 CC regulation of erythrocyte differentiation and the maintenance of a
 CC physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 CC and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
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 CC -----
 DR EMBL; M12482; AAA37568.1; -;
 DR EMBL; M12930; AAA37570.1; -;
 DR EMBL; AF312033; AAK28825.1; -;
 DR EMBL; Y11971; CAA72707.1; -;
 DR PIR; A24902; A24902.
 DR HSSP; P01588; 1CN4.
 DR MGD; MGI:95407; Epo.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 192
 FT DISULFID 33 187
 FT CARBOHYD 50 50
 FT CARBOHYD 64 64
 FT CARBOHYD 109 109
 SQ SEQUENCE 192 AA; 21365 MW; 65F94E214B0DEF2E CRC64;
 Query Match 77.6%; Score 694; DB 1; Length 192;
 Best Local Similarity 80.1%; Pred. No. 7.3e-57;
 Matches 133; Conservative 14; Mismatches 19; Indels 0; Gaps 0;
 QY 9 APRILICDSRVLYLEAEKAEENITTCGAHCSLNENITVPTKYNFYAKRMEYQQA 68
 DB 27 APRILICDSRVLYLEAEKAEENITTCGAHCSLNENITVPTKYNFYAKRMEVEEQA 86
 QY 69 VEVWQGLALLSEAVLQGALLVNSQWPEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 128
 DB 87 IEVWQGLSLLSEAILQALANSQPPETLQHLVDKAVSGLSRLTTLRALGAQKEAIS 146
 QY 129 PDAA-SAAPLRTITADTFRKLVNFRVSNFLRGKLYTGACRTGDR 174
 DB 147 PPDTPPAPLRLTITVDTFCKLFRVYANFLRGKLYTGACRTGDR 192

RESULT 12
 EPO SHEEP
 ID EPO SHEEP STANDARD; PRT; 194 AA.
 AC P33709; Q28572;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=EPO;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93351736; PubMed=8349021;
 RA Fu P., Evans B., Lim G.B., Moritz K., Wintour M.E.;
 RT "The sheep erythropoietin gene: molecular cloning and effect of
 RT hemorrhage on plasma erythropoietin and renal/liver messenger RNA in
 RT adult sheep";
 RL Mol. Cell. Endocrinol. 93:107-116 (1993).
 RN [2]
 RP SEQUENCE OF 4-194 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,

RA Czelusniak J., Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 RL sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 CC regulation of erythrocyte differentiation and the maintenance of a
 CC physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 CC and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
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DR EMBL; Z24681; CAAB0848.1; -;
 DR EMBL; LI0610; AAA31518.1; -;
 DR PIR; I46401; I46401.
 DR HSSP; P01588; 1CN4.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 194
 FT DISULFID 34 189
 FT DISULFID 56 60
 FT CARBOHYD 51 51
 FT CARBOHYD 65 65
 FT CARBOHYD 110 110
 FT CONFLICT 16 16 F -> L (in Ref. 2).
 FT CONFLICT 108 108 L -> P (in Ref. 2).
 SQ SEQUENCE 194 AA; 21335 MW; C025AAB0528131A9 CRC64;

Query Match 77.2%; Score 690.5; DB 1; Length 194;
 Best Local Similarity 82.0%; Pred. No. 1.6e-56;
 Matches 137; Conservative 9; Mismatches 20; Indels 1; Gaps 1;
 QY 9 APPRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPTKYNFYAWKMEVQQA 68
 DB 28 APPRLICDSRVLELYLEAKEAENATMGCAEGCSFSENITVPTKYNFYAWKMEVQQA 87
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGRLSLTLRLALGAQKEAIS 128
 DB 88 LEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGRLSLTLRLALGAQKEAIS 147
 QY 129 PDAA-SAAPLRTITADTFKLFVYVSNFLRGKLYTGACRTGDR 174
 DB 148 LPDAPSAAPLRTITADTFKLFVYVSNFLRGKLYTGACRTGDR 194

RESULT 13
 Q9GKA2 PRELIMINARY; PRT; 195 AA.
 ID Q9GKA2
 AC Q9GKA2
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Erythropoietin.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21290682; PubMed=11396976;
 RA Villalta A., Wu D., Margalith M., Hobart P.;
 RT "Rabbit EPO gene and cDNA: expression of rabbit EPO after
 RT intramuscular injection of pDNA.";
 RL Biochem. Biophys. Res. Commun. 284:823-827(2001).
 DR EMBL; AF290944; AAG36962.1; -;
 DR HSSP; P01588; 1CN4.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 SQ SEQUENCE 195 AA; 21025 MW; 1F1DC7F403A303EC CRC64;

Query Match 76.7%; Score 685.5; DB 2; Length 195;
 Best Local Similarity 81.4%; Pred. No. 4.7e-56;
 Matches 136; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
 QY 9 APPRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPTKYNFYAWKMEVQQA 68
 DB 29 APPRLICDSRVLELYLEAKEAENITMGCAEGCSLGENITVPTKYNFYAWKMEVQQA 88
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGRLSLTLRLALGAQKEAIS 128
 DB 89 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGRLSLTLRLALGAQKEAIS 148
 QY 129 PDAA-SAAPLRTITADTFKLFVYVSNFLRGKLYTGACRTGDR 174
 DB 149 PPEAASSAAPLRTVAADTLCKLFRIYSNLFRLGKLYTGACRRGDR 195

RESULT 14
 Q9GKA3 PRELIMINARY; PRT; 195 AA.
 ID Q9GKA3
 AC Q9GKA3
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Erythropoietin.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21290682; PubMed=11396976;
 RA Villalta A., Wu D., Margalith M., Hobart P.;
 RT "Rabbit EPO gene and cDNA: expression of rabbit EPO after
 RT intramuscular injection of pDNA.";
 RL Biochem. Biophys. Res. Commun. 284:823-827(2001).
 DR EMBL; AF290943; AAG36961.1; -;
 DR PIR; JC7699; JC7699.
 DR HSSP; P01588; 1CN4.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 SQ SEQUENCE 195 AA; 21053 MW; 0999DA7D852713F3 CRC64;
 Query Match 76.7%; Score 685.5; DB 2; Length 195;
 Best Local Similarity 81.4%; Pred. No. 4.7e-56;

```
Matches 136; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
QY 9 APPRLICDSVLRVLEAEAEENITTCGAHCSLNENITVPTKVNIFYAKRMVEVQQA 68
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 29 APPRLICDSVLRVLEAEAEENITTCGAHCSLNENITVPTKVNIFYAKRMVEVQQA 88
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPEQLQHVVDKAVSGLSLTLTLRALGAQKEAIS 128
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 89 VEVWQGLALLSEAVLRGQALLVNSQWPEQLQHVVDKAVSGLSLTLTLRALGAQKEAIS 148
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 129 PPDA--AAPLRTITADTFKLPVYSNPLRGKLYTGACRTGDR 174
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 149 PPEANSAAPLRTVAADTLCKLFRIVSNFLRGKLYTGACRRGDR 195
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
EPO_PIG STANDARD; PRT; 190 AA.
ID EPO_PIG AC P49157;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Erythropoietin precursor (Fragment).
GN Name=EPO;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
RA Czelusniak J., Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
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CC -----
DR EMBL; LI0607; AAA31029.1; -
DR F1R; I46578; I46578.
DR HSSP; P01588; 1CN4.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythropn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT NON_TER 1
FT SIGNAL <1 22 Potential.
FT CHAIN 23 190 Erythropoietin.
FT DISULFID 29 185 By similarity.
FT DISULFID 51 55 By similarity.
FT CARBOHYD 46 46 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 60 60 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 105 105 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 168 168 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 190 AA; 20888 MW; A75BD6CCE5077E2A CRC64;
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Query Match 76.4%; Score 683; DB 1; Length 190;
Best Local Similarity 82.1%; Pred. No. 7.8e-56;
Matches 138; Conservative 7; Mismatches 21; Indels 2; Gaps 1;
QY 9 APPRLICDSVLRVLEAEAEENITTCGAHCSLNENITVPTKVNIFYAKRMVEVQQA 68
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 APPRLICDSVLRVLEAEAEENITTCGAHCSLNENITVPTKVNIFYAKRMVEVQQA 82
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPEQLQHVVDKAVSGLSLTLTLRALGAQKEAIS 128
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 MEVWQGLALLSEAILQOALLANSSQFSEALQHLHVDKAVSGLSLTLTLRALGAQKEAIP 142
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 129 PPDA--ASAPLRTITADTFKLPVYSNPLRGKLYTGACRTGDR 174
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 143 LPDASPSSATPLRTFAVDTLCKLFRIVSNFLRGKLYTGACRRRDR 190
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Search completed: November 19, 2004, 21:10:58
Job time : 105.996 secs

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OM protein - protein search, using sw model

Run on: November 19, 2004, 20:57:38 ; Search time 59,4932 Seconds
(without alignments)
1019,028 Million cell updates/sec

Title: US-10-014-363-4

Perfect score: 869

Sequence: 1 APPAPRLICDSRLVRLYL.....NFLRGLKLYTGACRTGDR 169

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	869	100.0	169	5	ABB77899	Abb77899 Amino aci
2	869	100.0	196	5	ABB77902	Abb77902 Amino aci
3	856.5	98.6	174	5	ABB77898	Abb77898 Amino aci
4	856.5	98.6	174	5	ABB77900	Abb77900 Amino aci
5	856.5	98.6	201	5	ABB77901	Abb77901 Amino aci
6	856.5	98.6	201	5	ABB77903	Abb77903 Amino aci
7	853	98.2	205	8	ADJ71846	Adj71846 Non-glyco
8	851	97.9	166	1	AA70398	Aap70398 Sequence
9	851	97.9	166	2	AA233593	Aar23593 Recombina
10	851	97.9	166	2	AA58404	Aaw58404 Human ery
11	851	97.9	166	2	AAW77780	Aaw77780 Human EPO
12	851	97.9	166	3	ABB07030	Abb07030 Modified
13	851	97.9	166	4	ABB83622	Abb83622 Protein #
14	851	97.9	166	4	AA502641	Aae02641 Human ery
15	851	97.9	166	4	AA566698	Aab66698 Human ery
16	851	97.9	166	5	ABG92101	Abg92101 Human ery
17	851	97.9	166	5	AAW53062	Aam53062 Human ery
18	851	97.9	166	5	ABB77897	Abb77897 Amino aci
19	851	97.9	166	5	AD565661	Adg56561 Human ery
20	851	97.9	166	6	ABR39996	Abr39996 Human ery
21	851	97.9	166	6	ABR57500	Abr57500 Human ery
22	851	97.9	166	7	ADF70839	Adf70839 Human ery
23	851	97.9	166	8	ADL92150	Adl92150 Erythro
24	851	97.9	166	8	ADK70564	Adk70564 Human ery
25	851	97.9	166	8	ADL88867	Adl88867 Human cyt

ALIGNMENTS

RESULT 1

ABB77899
ID ABB77899 standard; protein; 169 AA.
XX
AC ABB77899;
XX
DT 07-OCT-2002 (first entry)
XX
DE Amino acid sequence of a modified human erythropoietin (EPO).
XX
KW Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
KW red blood cell production; anaemia; chronic renal failure;
KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
KW committed erythroid progenitor.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Cleavage-site 1..3
FT Protein /note= "proteolytic cleavage site"
FT Protein 4..174
FT Protein /note= "EPO protein"
XX
WO200249673-A2.
XX
PD 27-JUN-2002.
XX
PF 08-DEC-2001; 2001WO-EP014434.
XX
PR 20-DEC-2000; 2000EP-00127891.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
PI Wozny M;
XX
DR WPI; 2002-566640/60.
XX
PT Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
PT useful for treating diseases correlated with anemia in chronic renal
PT failure patients and acquired immunodeficiency syndrome.
XX
PS Disclosure; Page 39; 40pp; English.
XX
CC The present sequence represents a modified human erythropoietin (EPO)
CC protein. The EPO was extended at the N-terminal by a proteolytic cleavage
CC site. it was used to produce conjugates of the invention. The

26	851	97.9	166	8	ADL06781	Adl06781 Human 166
27	851	97.9	166	8	ADO59416	Ado59416 Human 166
28	851	97.9	167	1	AA50299	Aap50299 Human rec
29	851	97.9	167	1	AA50298	Aap50298 Human rec
30	851	97.9	188	1	AA60599	Aap60599 Clone lam
31	851	97.9	188	1	AA681195	Aap81195 Erythro
32	851	97.9	193	1	AA50300	Aap50300 Human ery
33	851	97.9	193	1	AA60597	Aap60597 Clone lam
34	851	97.9	193	1	AA60597	Aap60597 Clone lam
35	851	97.9	193	1	AA60597	Aap60597 Clone lam
36	851	97.9	193	2	AA65499	Aar65499 Human pre
37	851	97.9	193	2	AA71137	Aar71137 Human ery
38	851	97.9	193	2	AA74141	Aar74141 Human ery
39	851	97.9	193	2	AA81982	Aar81982 Human ery
40	851	97.9	193	2	AA98397	Aar98397 Human ery
41	851	97.9	193	3	AA433398	Aay43398 Human ery
42	851	97.9	193	3	AA94530	Aay94530 Human ery
43	851	97.9	193	3	AA93638	Aay93638 Amino aci
44	851	97.9	193	3	AA99704	Aay99704 Human non
45	851	97.9	193	4	AA34978	Aab34978 Human ery
					AA85573	Aab85573 Human ery

CC specification describes a conjugate comprising an EPO glycoprotein having
 CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 CC or a rearrangement of a glycosylation site). The glycoprotein is
 CC covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 CC has in vivo biological activity of causing bone marrow cells to increase
 CC production of reticulocytes and red blood cells. The conjugate increased
 CC circulating half-life and plasma residence time, decreased clearance, when
 CC compared to unmodified EPO. The EPO conjugate is useful for preparing
 CC medicaments for the treatment and prophylaxis of diseases correlated with
 CC anaemia in chronic renal failure patients (CRF), acquired
 CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow
 XX
 SQ Sequence 169 AA;

Query Match 100.0%; Score 869; DB 5; Length 169;
 Best Local Similarity 100.0%; Pred. No. 8.1e-88;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APPAPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAWKMEVG 60
 DB 1 APPAPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAWKMEVG 60
 QY 61 QOAVEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSRLTLLRALGAQKE 120
 DB 61 QOAVEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSRLTLLRALGAQKE 120
 QY 121 AISPDPDASAAPLRTITADTFRKLFRVYSNFRGLKLYTGEACRTGDR 169
 DB 121 AISPDPDASAAPLRTITADTFRKLFRVYSNFRGLKLYTGEACRTGDR 169

RESULT 2
 ABB77902
 ID ABB77902 standard; protein; 196 AA.
 XX
 AC ABB77902;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Amino acid sequence of a modified human erythropoietin (EPO).
 XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 XX red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.
 XX
 OS Synthetic.
 OS Homo sapiens.

Key Location/Qualifiers
 FT Peptide 1..27 "secretion signal peptide"
 FT Cleavage-site 28..30 "proteolytic cleavage site"
 FT Protein 31..196 "EPO protein"
 XX
 PN WO200249673-A2.
 XX
 PD 27-JUN-2002.
 XX
 XX 08-DEC-2001; 2001WO-EP014434.
 XX
 XX 20-DEC-2000; 2000EP-00127891.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA
 XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 PI

PI Wozny M;
 XX
 DR WPI; 2002-566640/60.
 DR N-PSDB; ABL59290.
 XX
 PT Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 PT useful for treating diseases correlated with anemia in chronic renal
 PT failure patients and acquired immunodeficiency syndrome.
 XX
 PS Disclosure; Fig 4; 40pp; English.

XX The present sequence represents a modified human erythropoietin (EPO)
 CC protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 CC site. It was used to produce conjugates of the invention. The
 CC specification describes a conjugate comprising an EPO glycoprotein having
 CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 CC or a rearrangement of a glycosylation site). The glycoprotein is
 CC covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 CC has in vivo biological activity of causing bone marrow cells to increase
 CC production of reticulocytes and red blood cells. The conjugate increased
 CC circulating half-life and plasma residence time, decreased clearance, when
 CC compared to unmodified EPO. The EPO conjugate is useful for preparing
 CC medicaments for the treatment and prophylaxis of diseases correlated with
 CC anaemia in chronic renal failure patients (CRF), acquired
 CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow
 XX
 SQ Sequence 196 AA;

Query Match 100.0%; Score 869; DB 5; Length 196;
 Best Local Similarity 100.0%; Pred. No. 1e-87;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APPAPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAWKMEVG 60
 DB 28 APPAPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAWKMEVG 87
 QY 61 QOAVEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSRLTLLRALGAQKE 120
 DB 88 QOAVEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSRLTLLRALGAQKE 147
 QY 121 AISPDPDASAAPLRTITADTFRKLFRVYSNFRGLKLYTGEACRTGDR 169
 DB 148 AISPDPDASAAPLRTITADTFRKLFRVYSNFRGLKLYTGEACRTGDR 196

RESULT 3
 ABB77898
 ID ABB77898 standard; protein; 174 AA.
 XX
 AC ABB77898;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Amino acid sequence of a modified human erythropoietin (EPO).
 XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Cleavage-site 1..8 "proteolytic cleavage site"
 FT Protein 9..174 "EPO protein"
 FT

XX WO200249673-A2.
 XX
 XX
 XX PD 27-JUN-2002.
 XX
 XX PF 08-DEC-2001; 2001WO-EP014434.
 XX PR 20-DEC-2000; 2000EP-00127891.
 XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX PI Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 XX Wozny M;
 XX WPI; 2002-566640/60.
 XX
 XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 XX useful for treating diseases correlated with anemia in chronic renal
 XX failure patients and acquired immunodeficiency syndrome.
 XX
 XX Disclosure; Page 38-39; 40pp; English.
 XX
 XX The present sequence represents a modified human erythropoietin (EPO)
 XX protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 XX site. It was used to produce conjugates of the invention. The
 XX specification describes a conjugate comprising an EPO glycoprotein having
 XX an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 XX analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 XX or a rearrangement of a glycosylation site). The glycoprotein is
 XX covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 XX has in vivo biological activity of causing bone marrow cells to increase
 XX production of reticulocytes and red blood cells. The conjugate increased
 XX circulating half-life and plasma residence time, decreased clearance,
 XX increased clinical activity in vivo, improved potency and stability, when
 XX compared to unmodified EPO. The EPO conjugate is useful for preparing
 XX medicaments for the treatment and prophylaxis of diseases correlated with
 XX anaemia in chronic renal failure patients (CRF), acquired
 XX immunodeficiency syndrome (AIDS) and for treating cancer patients
 XX undergoing chemotherapy. It is also useful for treating patients by
 XX stimulating the division and differentiation of committed erythroid
 XX progenitors in the bone marrow
 XX
 XX Sequence 174 AA;
 XX
 XX Query Match 98.6%; Score 856.5; DB 5; Length 174;
 XX Best Local Similarity 97.1%; Pred. No. 28-86;
 XX Matches 169; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
 XX
 XX 1 APP-----APPRILCDSRVLLRYLLEAKEAENITTCGAHCSLNENITVPDTKVNFWYAWK 55
 XX 1 APPRIEGRAPPRILCDSRVLLRYLLEAKEAENITTCGAHCSLNENITVPDTKVNFWYAWK 60
 XX
 XX 56 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTTLLRAL 115
 XX 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTTLLRAL 120
 XX
 XX 116 GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 169
 XX 121 GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 174
 XX
 XX RESULT 4
 XX ABB77900
 XX ID ABB77900 standard; protein; 174 AA.
 XX AC ABB77900;
 XX XX
 XX 07-OCT-2002 (first entry)
 XX DE Amino acid sequence of a modified human erythropoietin (EPO).
 XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 XX red blood cell production; anaemia; chronic renal failure;
 XX

acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 committed erythroid progenitor.
 Synthetic.
 Homo sapiens.
 Key Location/Qualifiers
 Cleavage-site 1..8
 /note= "proteolytic cleavage site"
 Protein 9..174
 /note= "EPO protein"
 WO200249673-A2.
 27-JUN-2002.
 08-DEC-2001; 2001WO-EP014434.
 20-DEC-2000; 2000EP-00127891.
 (HOFF) HOFFMANN LA ROCHE & CO AG F.
 Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 Wozny M;
 WPI; 2002-566640/60.
 Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 useful for treating diseases correlated with anemia in chronic renal
 failure patients and acquired immunodeficiency syndrome.
 Disclosure; Page 39-40; 40pp; English.
 The present sequence represents a modified human erythropoietin (EPO)
 protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 site. It was used to produce conjugates of the invention. The
 specification describes a conjugate comprising an EPO glycoprotein having
 an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 or a rearrangement of a glycosylation site). The glycoprotein is
 covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 has in vivo biological activity of causing bone marrow cells to increase
 production of reticulocytes and red blood cells. The conjugate increased
 circulating half-life and plasma residence time, decreased clearance,
 increased clinical activity in vivo, improved potency and stability, when
 compared to unmodified EPO. The EPO conjugate is useful for preparing
 medicaments for the treatment and prophylaxis of diseases correlated with
 anaemia in chronic renal failure patients (CRF), acquired
 immunodeficiency syndrome (AIDS) and for treating cancer patients
 undergoing chemotherapy. It is also useful for treating patients by
 stimulating the division and differentiation of committed erythroid
 progenitors in the bone marrow
 Sequence 174 AA;
 Query Match 98.6%; Score 856.5; DB 5; Length 174;
 Best Local Similarity 97.1%; Pred. No. 28-86;
 Matches 169; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
 1 APP-----APPRILCDSRVLLRYLLEAKEAENITTCGAHCSLNENITVPDTKVNFWYAWK 55
 1 APPRIEGRAPPRILCDSRVLLRYLLEAKEAENITTCGAHCSLNENITVPDTKVNFWYAWK 60
 56 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTTLLRAL 115
 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTTLLRAL 120
 116 GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 169
 121 GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 174
 RESULT 5

ABB77901
 ID ABB77901 standard; protein; 201 AA.
 XX
 AC ABB77901;
 DT 07-OCT-2002 (first entry)
 XX
 DE Amino acid sequence of a modified human erythropoietin (EPO).
 XX
 KW Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide
 FT Location/Qualifiers
 FT 1..27 "secretion signal peptide"
 FT Cleavage-site
 FT 28..35 /note= "proteolytic cleavage site"
 FT Protein
 FT 36..201 /note= "EPO protein"
 FT WO200249673-A2.
 XX
 PD 27-JUN-2002.
 XX
 PF 08-DEC-2001; 2001WO-EP014434.
 XX
 PR 20-DEC-2000; 2000EP-00127891.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischler W;
 PI Wozny M;
 XX
 XX WPI; 2002-566640/60.
 DR N-PSDB; ABL59289.
 XX
 PT Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 PT useful for treating diseases correlated with anemia in chronic renal
 PT failure patients and acquired immunodeficiency syndrome.
 XX
 PS Disclosure; Fig 3; 40pp; English.
 XX
 CC The present sequence represents a modified human erythropoietin (EPO)
 CC protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 CC site. It was used to produce conjugates of the invention. The
 CC specification describes a conjugate comprising an EPO glycoprotein having
 CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 CC or a rearrangement of a glycosylation site). The glycoprotein is
 CC covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 CC has in vivo biological activity of causing bone marrow cells to increase
 CC production of reticulocytes and red blood cells. The conjugate increased
 CC circulating half-life and plasma residence time, decreased clearance,
 CC compared to unmodified EPO. The EPO conjugate is useful for preparing
 CC medicaments for the treatment and prophylaxis of diseases correlated with
 CC anaemia in chronic renal failure patients (CRF), acquired
 CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow
 XX
 XX Sequence 201 AA;
 Query Match 98.6%; Score 856.5; DB 5; Length 201;
 Best Local Similarity 97.1%; Pred. No. 2.5e-86;
 Matches 169; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

1 APP-----APPLRICDSRVLYLEAKAEANITTCABHCSLNENITVPDTKVNFAWK 55
 |||||
 28 APPRIEGRAPPLRICDSRVLYLEAKAEANITTCABHCSLNENITVPDTKVNFAWK 87
 |||||
 56 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSSQWPEPLQLHVDKAVSGLSITLLRAL 115
 |||||
 88 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSSQWPEPLQLHVDKAVSGLSITLLRAL 147
 |||||
 116 GAQKAISPDDAASAPLRTITADTFKLFVYVSNFLRGKLYTGEACRTGDR 169
 |||||
 148 GAQKAISPDDAASAPLRTITADTFKLFVYVSNFLRGKLYTGEACRTGDR 201
 |||||

RESULT 6
 ABB77903
 ID ABB77903 standard; protein; 201 AA.
 XX
 AC ABB77903;
 DT 07-OCT-2002 (first entry)
 XX
 DE Amino acid sequence of a modified human erythropoietin (EPO).
 XX
 KW Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide
 FT Location/Qualifiers
 FT 1..27 "secretion signal peptide"
 FT Cleavage-site
 FT 28..35 /note= "proteolytic cleavage site"
 FT Protein
 FT 36..201 /note= "EPO protein"
 FT WO200249673-A2.
 XX
 PD 27-JUN-2002.
 XX
 PF 08-DEC-2001; 2001WO-EP014434.
 XX
 PR 20-DEC-2000; 2000EP-00127891.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischler W;
 PI Wozny M;
 XX
 XX WPI; 2002-566640/60.
 DR N-PSDB; ABL59291.
 XX
 PT Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 PT useful for treating diseases correlated with anemia in chronic renal
 PT failure patients and acquired immunodeficiency syndrome.
 XX
 PS Disclosure; Fig 5; 40pp; English.
 XX
 CC The present sequence represents a modified human erythropoietin (EPO)
 CC protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 CC site. It was used to produce conjugates of the invention. The
 CC specification describes a conjugate comprising an EPO glycoprotein having
 CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 CC or a rearrangement of a glycosylation site). The glycoprotein is
 CC covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 CC has in vivo biological activity of causing bone marrow cells to increase
 CC production of reticulocytes and red blood cells. The conjugate increased
 CC circulating half-life and plasma residence time, decreased clearance,
 CC compared to unmodified EPO. The EPO conjugate is useful for preparing
 CC medicaments for the treatment and prophylaxis of diseases correlated with
 CC anaemia in chronic renal failure patients (CRF), acquired
 CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLYRLLLEAKAENITTCGAHCSSLNENITVPDTKVNFYAWKRMVEVQQA 63
Db 1 APPRLICDSRVLYRLLLEAKAENITTCGAHCSSLNENITVPDTKVNFYAWKRMVEVQQA 60

QY 64 VEVWQGLALLSVAVLRGQALLVNSSQPWEPLQHVDAKAVSGLSLTTLLRALGAOKEATS 123
Db 61 VEVWQGLALLSVAVLRGQALLVNSSQPWEPLQHVDAKAVSGLSLTTLLRALGAOKEATS 120

QY 124 PDDAASAPLRITITADTRFKLFRVYSNFRGLKLYTGACRTGDR 169
Db 121 PDDAASAPLRITITADTRFKLFRVYSNFRGLKLYTGACRTGDR 166

RESULT 9
ID AAR23593
XX AAR23593 standard; protein; 166 AA.
AC AAR23593;
XX
DT 20-OCT-1992 (first entry)
DE Recombinant hematopoietic molecule portion 2.
XX
KW Erythropoietin; EPO; erythrocytes; IL-3; hematopoiesis.
XX Homo sapiens.
XX WO9206116-A.
XX
PD 16-APR-1992.
XX
PF 26-SEP-1991; 91WO-US007053.
XX
PR 28-SEP-1990; 90US-00589958.
XX
PA (ORTH) ORTHO PHARM CORP.
XX
PI Rosen JI;
XX
XX WPI; 1992-150819/18.
XX
XX Recombinant haematopoietic molecules useful in treating anaemia(s) -
PT comprise IL3 or GM-CSF and EPO, G-CSF, IL-5 or M-CSF and has early and
PT later myeloid differentiation activity.
XX
XX Disclosure; Page 32; 82pp; English.

CC This protein sequence given comprises the entire amino acid sequence of
CC human erythropoietin (EPO). EPO leads to the maturation of erythrocytes
CC and is therefore designated as a late myeloid differentiation factor
CC (MDF). Within the scope of the invention hybrid molecules were produced
CC which contain at least a portion of an early MDF and at least a portion
CC of a late MDF covalently linked. The EPO sequence given is effective
CC within the scope of the invention in full or in a truncated version.
CC Amino acids 7-161 act as a late MDF when recombined with an early MDF eg.
CC IL-3. These compounds can be used to promote hematopoiesis in a patient.
CC The bonding of the early and late factors allows a very high conc. of
CC late MDF at the surface of a cell which the early MDF is bound. It also
CC allows the early MDA to act more specifically to stimulate only the
CC desired lineage, thus reducing undesirable effects. These compounds are
CC useful for treating anemias of various origins eg. renal failure and
CC AIDS. It is easier to produce and administer one recombinant molecule
CC rather than two separate molecules

XX
XX Sequence 166 AA;

Query Match 97.9%; Score 851; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.8e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLYRLLLEAKAENITTCGAHCSSLNENITVPDTKVNFYAWKRMVEVQQA 63

Db 1 APPRLICDSRVLYRLLLEAKAENITTCGAHCSSLNENITVPDTKVNFYAWKRMVEVQQA 60

QY 64 VEVWQGLALLSVAVLRGQALLVNSSQPWEPLQHVDAKAVSGLSLTTLLRALGAOKEATS 123
Db 61 VEVWQGLALLSVAVLRGQALLVNSSQPWEPLQHVDAKAVSGLSLTTLLRALGAOKEATS 120

QY 124 PDDAASAPLRITITADTRFKLFRVYSNFRGLKLYTGACRTGDR 169
Db 121 PDDAASAPLRITITADTRFKLFRVYSNFRGLKLYTGACRTGDR 166

RESULT 10
ID AAW58404
XX AAW58404 standard; protein; 166 AA.
AC AAW58404;
XX
DT 12-OCT-1998 (first entry)
XX
DE Human erythropoietin.
XX
KW Erythropoietin receptor agonist; EPO; human; anaemia;
KW haematopoietic deficiency; red blood cell; erythroid progenitor;
KW bone marrow suppression.
XX
XX Homo sapiens.
XX WO9818926-A1.
XX
PD 07-MAY-1998.
XX
PF 23-OCT-1997; 97WO-US018703.
XX
PR 25-OCT-1996; 96US-0034044P.
XX
XX (SEAR) SEARLE & CO G D.
XX
XX McWherter CA, Feng Y, Summers N;
XX
XX WPI; 1998-272221/24.
DR N-PSDB; AAV31031.
XX
XX Human erythropoietin receptor agonist polypeptide - used to stimulate the
PT production of red blood cells in a patient.
XX
XX Claim 1; Page 93; 112pp; English.

CC A claimed human erythropoietin (EPO) receptor agonist polypeptide
CC comprises a modified EPO amino acid sequence given in AAW58404, where (a)
CC optionally 1-6 amino acids from the N-terminus and 1-5 from the C-
CC terminus can be deleted, (b) the N-terminus is joined to the C-terminus
CC directly or through a linker (see AAW58405-12) capable of joining the N-
CC terminus to the C-terminus, (c) there are new C- and N-termini at any two
CC consecutive amino acids from amino acids 23-24 to 38-39, 40-41 to 41-42,
CC 43-44 to 48-49, 50-51 to 57-58, 77-78 to 82-83, 84-85 to 88-89, and 108-
CC 109 to 131-132, and (d) optionally the agonist polypeptide is preceded by
CC Met, Ala, or Met-Ala. 60 Of these circularly permuted EPO receptor
CC agonists (see AAW58413-72) are claimed. Also claimed are: nucleic acid
CC molecules (see AAV30971-V31030) encoding novel EPO receptor agonists; a
CC method of producing an EPO receptor agonist using transfection or
CC transfected host cells; and methods for stimulating the production of
CC haematopoietic cells, for selective ex vivo expansion of erythroid
CC progenitors, and treating patients having a haematopoietic disorder using
CC the EPO receptor agonists. The EPO receptor agonists retain one or more
CC activities of native EPO and may also show improved haematopoietic cell-
CC stimulating activity and/or an improved activity profile which may
CC include reduction of undesirable biological activities associated with
CC native EPO and/or have improved physical properties such as increased
CC solubility, stability and refold efficiency

XX
XX Sequence 166 AA;

FT	Misc-difference	41. .42	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	42. .43	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	43. .44	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	44. .45	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	45. .46	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	46. .47	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	47. .48	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	48. .49	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	49. .50	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	50. .51	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	51. .52	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	52. .53	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	53. .54	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	54. .55	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	55. .56	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	56. .57	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	57. .58	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	77. .78	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	78. .79	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	79. .80	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	81. .82	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	82. .83	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	84. .85	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	85. .86	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	86. .87	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	87. .88	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	88. .89	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	108. .109	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	109. .110	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	110. .111	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	111. .112	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	112. .113	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	113. .114	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	114. .115	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	115. .116	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	116. .117	/note= "possible positions of new C- and N-termini"
FT	Misc-difference	117. .118	/note= "possible positions of new C- and N-termini"

FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 118. .119
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 119. .120
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 120. .121
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 121. .122
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 122. .123
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 123. .124
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 124. .125
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 125. .126
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 126. .127
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 127. .128
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 128. .129
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 129. .130
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 130. .131
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 131. .132
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 162. .166
FT /note= "1-5 amino acids of the C-terminus are optionally
FT deleted"
FT
FT
XX WO9817810-A2.
XX
XX 30-APR-1998.
XX
XX 23-OCT-1997; 97WO-US020037.
XX
XX 25-OCT-1996; 96US-0029629P.
XX
XX (SEAR) SEARLE & CO G D.
XX
XX McWhorter CA, Feng Y, McKearn JP, Summers NL, Staten NR;
XX Streeter PR, Minnerly JC, Minster NI, Moulfe SL;
XX
XX WPI; 1998-261504/23.
XX
XX Multi-functional chimeric haematopoietic receptor agonist - useful to
XX treat haematopoietic disorders, tumours, infections or autoimmune
XX diseases.
XX
XX Claim 1; Page 762; 841pp; English.
XX
XX A human erythropoietin (EPO) receptor agonist polypeptide comprises a
XX modified EPO amino acid sequence of the formula provided in AAW7780, in
XX which the N-terminus is joined to the C-terminus directly or via a
XX linker, the polypeptide having new C- and N-termini at one of the
XX positions indicated. Novel claimed multi-functional chimeric
XX haematopoietic receptor agonists (see AAW7781-22) have the formula R1-L1
XX -R2, R2-L1-R1, R1-R2 or R2-R1, where L1 is a linker and R1 and R2 are
XX independently selected from: (a) the human EPO receptor agonist; (b) a
XX human stem cell factor receptor agonist polypeptide (see AAW7781); (c) a
XX human f1t-3 receptor agonist polypeptide (see AAW7782); (d) a modified
XX human granulocyte colony stimulating factor (G-CSF) polypeptide (see
XX AAW7783); (e) modified human interleukin-3 polypeptide (see AAW7784);
XX (f) modified human c-mpl ligand polypeptide (see AAW7785); and (g) a
XX factor selected from the group consisting of a CSF, a cytokine, a
XX lymphokine, an interleukin and a haematopoietic growth factor, provided
XX that at least R1 or R2 is selected from (a), (b) or (c) as above. The
XX multi-functional chimeric haematopoietic receptor agonist can be used to
XX stimulate the production of haematopoietic cells in a patient, for the ex
XX vivo expansion of haematopoietic cells, for the production of dendritic

Query Match 97.9%; Score 851; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.8e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APPRLICDSRVLELYLLEAKEAENITTCAGHCSSLNENITVPDTKKNFYAWKRMVEVQQA 63
DB 1 APPRLICDSRVLELYLLEAKEAENITTCAGHCSSLNENITVPDTKKNFYAWKRMVEVQQA 60
QY 64 VEVWQGLALLSEAVLRQALLVNSQWPPELOLHVDKAVSGLSLTLRLALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRQALLVNSQWPPELOLHVDKAVSGLSLTLRLALGAQKEAIS 120
QY 124 PPDASAAPLRTITADTFRKLFRVYSNFRGLKLYTGEACRTGDR 169
DB 121 PPDASAAPLRTITADTFRKLFRVYSNFRGLKLYTGEACRTGDR 166
RESULT 12
ABB07030
ID ABB07030 standard; protein; 166 AA.
XX AC ABB07030;
XX 21-JUN-2002 (first entry)
XX Modified erythropoietin related gene protein sequence.
XX DE Modified erythropoietin; EPO.
XX OS Unidentified.
XX PN KR145802-B1.
XX PD 01-AUG-1998.
XX PF 31-MAY-1994; 94KR-00012082.
XX PR 31-MAY-1994; 94KR-00012082.
XX PA (GLDS) LG CHEM CO LTD.
XX PI Kim C, Song Y, Lee T;
XX DR WPI; 2000-234250/20.
XX DR N-PSDB; ABL50878.
XX PT MODIFIED ERYTHROPOIETIN GENE AND EXPRESSION VECTORS THEREOF.
XX PS Disclosure; Page 14; 15pp; Korean.
XX CC The present invention describes modified erythropoietin (EPO) genes and
XX CC expression vectors comprising the genes. The present sequence represents
XX CC a protein sequence from the present invention
XX QY Sequence 166 AA;
Query Match 97.9%; Score 851; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.8e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APPRLICDSRVLELYLLEAKEAENITTCAGHCSSLNENITVPDTKKNFYAWKRMVEVQQA 63
DB 1 APPRLICDSRVLELYLLEAKEAENITTCAGHCSSLNENITVPDTKKNFYAWKRMVEVQQA 60
QY 64 VEVWQGLALLSEAVLRQALLVNSQWPPELOLHVDKAVSGLSLTLRLALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRQALLVNSQWPPELOLHVDKAVSGLSLTLRLALGAQKEAIS 120
QY 124 PPDASAAPLRTITADTFRKLFRVYSNFRGLKLYTGEACRTGDR 169
DB 121 PPDASAAPLRTITADTFRKLFRVYSNFRGLKLYTGEACRTGDR 166

RESULT 13

ABB83622
ID ABB83622 standard; protein; 166 AA.
XX
XX
AC ABB83622;
XX
DT 10-OCT-2002 (first entry)
XX
DE Protein #2 relating to modified erythropoietin glycoprotein.
XX
XX Erythropoietin glycoprotein; anaemia; chronic renal failure; AIDS;
KW cancer.
XX
XX
OS Unidentified.
XX
PN NO200003372-A.
XX
PD 03-JAN-2001.
XX
PF 28-JUN-2000; 2000NO-00003372.
XX
PR 02-JUL-1999; 99US-0142254P.
PR 23-AUG-1999; 99US-0150225P.
PR 31-AUG-1999; 99US-0151548P.
PR 17-NOV-1999; 99US-0166151P.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Bailon PS;
PI
XX
XX WPI; 2001-135308/14.
DR
XX
XX New conjugate having modified erythropoietin glycoprotein useful for
PT stimulating red blood cell production and for treating diseases
PT correlated with anemia in chronic renal failure, AIDS or cancer patients.
XX
XX Disclosure; Page 22-23; 30pp; Norwegian.
PS
XX
XX This invention relates to new conjugate having a modified erythropoietin
CC glycoprotein, useful for stimulating red blood cell production, and for
CC treating or preventing diseases correlated with anaemia in chronic renal
CC failure, AIDS or cancer patients. The present sequence is a protein
CC related to the invention
XX
SQ Sequence 166 AA;

Query Match 97.9%; Score 851; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.8e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APPRLICDSRVLELYLLEAKEAENITTCGAHCNSLNENITVPDTKVFYAWKRMVEVGOQA 63
DB 1 APPRLICDSRVLELYLLEAKEAENITTCGAHCNSLNENITVPDTKVFYAWKRMVEVGOQA 60
QY 64 VEVWQGLALLSVAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSRLTTLRLALGAOKEATS 123
DB 61 VEVWQGLALLSVAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSRLTTLRLALGAOKEATS 120
QY 124 PPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 169
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 166

RESULT 14

AAE02641
ID AAE02641 standard; protein; 166 AA.
XX
XX
AC AAE02641;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human erythropoietin (EPO) mature protein.

XX

KW Human; erythropoietin; EPO; antianaemic; nephrotrophic; anti-HIV;
KW vaccine; haemostatic; immunoglobulin; Ig; EPO deficient disease; anaemia;
KW renal failure; Human Immunodeficiency Virus; HIV;
KW haematopoietic growth factor.

OS Homo sapiens.

XX WO200136489-A2.

XX 25-MAY-2001.

XX 03-NOV-2000; 2000WO-EP010843.

XX 12-NOV-1999; 99US-0164855P.

XX (MERE) MERCK PATENT GMBH.

XX Hartmann A, Brandt S, Rieke E, Sobel C, Lo K, Way JC, Gillies S;

XX WPI; 2001-367563/38.

XX N-PSDB; AAD06893.

XX Novel modified erythropoietin forms such as fusion proteins, comprising
PT Fc portion of an immunoglobulin molecule and a target molecule having the
PT biological activity of erythropoietin forms.

XX Example 1; Page 22; 58pp; English.

XX The present sequence is human erythropoietin (EPO) mature protein. EPO
CC has improved biological activity and an extended serum half life greater
CC than 20 hours. The present invention relates to modified EPO forms such
CC as fusion proteins comprising a Fc portion of an immunoglobulin (Ig)
CC molecule and an EPO molecule (Fc-EPO). The Fc portion is fused covalently
CC through its C-terminus directly or indirectly to the EPO molecule, and
CC where the Fc portion as well as EPO portion may be modified or mutated.
CC The invention also relates to non-fused EPO molecules which have a
CC pattern of cysteines or disulphide bonding which is distinct from human
CC or animal EPO. Pharmaceutical compositions containing EPO are useful in
CC the treatment of EPO deficient diseases such as anaemia, renal failure,
CC HIV infection, blood loss and chronic disease that can be treated with
CC haematopoietic growth factor

XX Sequence 166 AA;

Query Match 97.9%; Score 851; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.8e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLELYLLEAKEAENITTCGAHCNSLNENITVPDTKVFYAWKRMVEVGOQA 63

DB 1 APPRLICDSRVLELYLLEAKEAENITTCGAHCNSLNENITVPDTKVFYAWKRMVEVGOQA 60

QY 64 VEVWQGLALLSVAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSRLTTLRLALGAOKEATS 123

DB 61 VEVWQGLALLSVAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSRLTTLRLALGAOKEATS 120

QY 124 PPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 169

DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 166

RESULT 15

AAE02698
ID AAE02698 standard; protein; 166 AA.

XX AAE02698;

XX 06-APR-2001 (first entry)

XX Human erythropoietin protein #2.

XX Erythropoietin; EPO; reticulocytes; red blood cell; ethylene glycol;

KW chronic renal failure; AIDS; cancer.

XX Homo sapiens.

PN WO200102017-A2.

XX 11-JAN-2001.

PD 28-JUN-2000; 2000WO-EP006009.

XX 02-JUL-1999; 99US-0142243P.

PR 05-AUG-1999; 99US-0147452P.

PR 30-AUG-1999; 99US-0151454P.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

PA Burg J, Hilger B, Josel H;

XX WPI; 2001-147051/15.

DR Novel erythropoietin-glycoprotein conjugate useful for treating diseases

PT correlated with anemia in chronic renal failure patients, AIDS and for

PT treating cancer, is linked to polyethylene glycol through linker.

XX Claim 19; Fig 2; 40pp; English.

XX The present invention relates to a conjugate comprising, human

CC erythropoietin glycoprotein (EPO) having at least one free amino group

CC and having in vivo biological activity of causing an increase the

CC production of reticulocytes and red blood cells, covalently linked to 1-3

CC lower-alkoxy poly(ethylene glycol) groups through a linker. The invention

CC is useful for preparation of medicaments for the treatment of prophylaxis

CC of disease correlated with anemia in chronic renal failure patients

CC (CRF), AIDS and for the treatment of cancer patients undergoing

CC chemotherapy

XX Sequence 166 AA;

SQ

Query Match 97.9%; Score 851; DB 4; Length 166;

Best Local Similarity 100.0%; Pred. No. 7.8e-86;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLEKAEKENITTCGAHCNENITVPTKYNFYAKKMEVGQQA 63

Db 1 APPRLICDSRVLEKAEKENITTCGAHCNENITVPTKYNFYAKKMEVGQQA 60

QY 64 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 123

Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120

QY 124 PPDAASAAPLRTITADTFKRLFRVSNFLRGKLYTGEACRTGDR 169

Db 121 PPDAASAAPLRTITADTFKRLFRVSNFLRGKLYTGEACRTGDR 166

Search completed: November 19, 2004, 21:05:44

Job time : 59.4932 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 21:00:09 ; Search time 17.325 Seconds
(without alignments)
646.913 Million cell updates/sec

Title: US-10-014-363-4

Perfect score: 869

Sequence:

1 APPAPPLICDSRVRLYLH.....NFLRGKLYTGACRTGDR 169

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pap.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pap.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pap.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pap.*
5: /cgn2_6/prodata/1/iaa/PCRU COMB.pap.*
6: /cgn2_6/prodata/1/iaa/backfile1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	97.9	166	1	US-08-318-193-70
2	851	97.9	166	3	US-09-604-871-2
3	851	97.9	166	4	US-09-604-938-2
4	851	97.9	166	4	US-09-462-941-2
5	851	97.9	166	5	PCT-US94-04361-37
6	851	97.9	193	1	US-07-903-220-1
7	851	97.9	193	2	US-08-883-795A-34
8	851	97.9	193	4	US-09-552-265B-4
9	848	97.6	412	4	US-09-366-009-34
10	848	97.6	412	4	US-08-809-156B-34
11	846	97.4	165	3	US-09-604-871-1
12	846	97.4	165	4	US-09-604-938-1
13	846	97.4	165	4	US-09-830-967-1
14	843	97.0	165	4	US-09-554-451-8
15	843	97.0	193	4	US-09-552-265B-2
16	839	96.5	193	4	US-09-552-265B-5
17	835	96.1	166	5	PCT-US94-04361-45
18	830	95.5	166	4	US-09-552-265B-30
19	830	95.5	166	4	US-09-552-265B-46
20	829	95.4	166	4	US-09-552-265B-22
21	829	95.4	166	4	US-09-552-265B-32
22	829	95.4	193	4	US-09-552-265B-38
23	829	95.4	193	4	US-09-552-265B-48
24	827	95.2	166	4	US-09-552-265B-20
25	827	95.2	166	4	US-09-552-265B-24
26	827	95.2	193	4	US-09-552-265B-36
27	827	95.2	193	4	US-09-552-265B-40

28 826 95.1 166 4 US-09-552-265B-26 Sequence 26, Appl
29 826 95.1 166 4 US-09-552-265B-31 Sequence 31, Appl
30 826 95.1 193 4 US-09-552-265B-42 Sequence 42, Appl
31 826 95.1 193 4 US-09-552-265B-47 Sequence 47, Appl
32 825 94.9 166 4 US-09-552-265B-18 Sequence 18, Appl
33 825 94.9 166 4 US-09-552-265B-23 Sequence 23, Appl
34 825 94.9 166 4 US-09-552-265B-28 Sequence 28, Appl
35 825 94.9 166 4 US-09-552-265B-33 Sequence 33, Appl
36 825 94.9 193 4 US-09-552-265B-34 Sequence 34, Appl
37 825 94.9 193 4 US-09-552-265B-39 Sequence 39, Appl
38 825 94.9 193 4 US-09-552-265B-44 Sequence 44, Appl
39 825 94.9 193 4 US-09-552-265B-49 Sequence 49, Appl
40 823 94.7 166 4 US-09-552-265B-21 Sequence 21, Appl
41 823 94.7 166 4 US-09-552-265B-25 Sequence 25, Appl
42 823 94.7 193 4 US-09-552-265B-37 Sequence 37, Appl
43 823 94.7 193 4 US-09-552-265B-41 Sequence 41, Appl
44 822 94.6 166 4 US-09-552-265B-27 Sequence 27, Appl
45 822 94.6 193 4 US-09-552-265B-43 Sequence 43, Appl

ALIGNMENTS

RESULT 1

US-08-318-193-70
; Sequence 70, Application US/08318193
; Patent No. 5641663
; GENERAL INFORMATION:
; APPLICANT: GARVIN, Robert T.
; APPLICANT: MALEK, Lawrence T.
; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
; TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,193
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,314
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; APPLICATION NUMBER: US 07/224,568
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 18740/116 CACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-318-193-70

Query Match 97.9%; Score 851; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.4e-98;

[illegible]

```

RESULT 2
US-09-604-871-2
; Sequence 2, Application US/09604871
; Patent No. 6340742
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Hilger, Bernd
; APPLICANT: Josef, Hans-Peter
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1098 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,871
; CURRENT FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/151,454
; PRIOR FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: 60/147,452
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/142,243
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-871-2

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	Query Match	97.9%	Score 851;	DB 3;	Length 166;
	Best Local Similarity	100.0%;	Prod. No. 4.4e-98;		
	Matches 166;	Conservative	0;	Mismatches	0;
				Indels	Gaps
				0;	0;
Qy	4	APPLRICDSRVLRVLLLEAKAEANITTCACGCHCSLNENITVPDTKNFYAWKRMVEVGQA	63		
Db	1	APPLRICDSRVLRVLLLEAKAEANITTCACGCHCSLNENITVPDTKNFYAWKRMVEVGQA	60		
Qy	64	VEVWQGLALLSEAVLRGQALLVNSSQWPEPQLQHVDKAVSGLSRLTTLIRALGAQKEAIS	123		
Db	61	VEVWQGLALLSEAVLRGQALLVNSSQWPEPQLQHVDKAVSGLSRLTTLIRALGAQKEAIS	120		
Qy	124	PPDAASAAPLRTITADTFPKLFRVYSNFIPLGKLKLYTGEACRTGDR	169		
Db	121	PPDAASAAPLRTITADTFPKLFRVYSNFIPLGKLKLYTGEACRTGDR	166		

```

RESULT 3
US-09-604-938-2
; Sequence 2, Application US/09604938
; Patent No. 6583272
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,938
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225

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; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-938-2

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	Query Match	97.9%;	Score 851;	DB 4;	Length 166;
	Best Local Similarity	100.0%;	Pred. No. 4.4e-98;		
	Matches 166;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	4	APPRLLCDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA	63		
Dd	1	APPRLLCDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVGGQA	60		
Qy	64	VEVWQGLALISEAVLRGQALLVNSSQPWEPLQHVDKAVSGLSLTTLLRALGAQKEAIS	123		
Dd	61	VEVWQGLALISEAVLRGQALLVNSSQPWEPLQHVDKAVSGLSLTTLLRALGAQKEAIS	120		
Qy	124	PPDAASAAPRTTATDFRKLFRVYSNFLRGKLYTGECARTGDR	169		
Dd	121	PPDAASAAPRTTATDFRKLFRVYSNFLRGKLYTGECARTGDR	166		

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RESULT 4
US-09-462-941-2
; Sequence 2, Application US/09462941
; Patent No. 6608183
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolden Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/09/462,941
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-462-941-2

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	Query Match	97.9%	Score 851	DB 4	Length 166	
	Best Local Similarity	100.0%	Prod. No. 4.4e-98			
	Matches 166	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	4	APPLIICDSRVLYRLYLEAKEAEENITTCGCAEHCSLINENITVPDTKVNFYAWKRWVEVGQQA	63			
DB	1	APPLIICDSRVLYRLYLEAKEAEENITTCGCAEHCSLINENITVPDTKVNFYAWKRWVEVGQQA	60			
QY	64	VEVWQGLALISEAVLRGQALLVNSSQWPEIQLQHVDKAVSGRLSLTILLRALGAKQEAIS	123			
DB	61	VEVWQGLALISEAVLRGQALLVNSSQWPEIQLQHVDKAVSGRLSLTILLRALGAKQEAIS	120			
QY	124	PPDAASAAPLTIITADTFRKLFRVYSNPLRGKLLKLYTGEACRTGDR	169			
DB	121	PPDAASAAPLTIITADTFRKLFRVYSNPLRGKLLKLYTGEACRTGDR	166			

RESULT 5
PCT-US94-04361-37
; Sequence 37, Application PC/TUS9404361
; GENERAL INFORMATION:
; APPLICANT: Brigham and Women's Hospital
; APPLICANT: 75 Francis Street
; APPLICANT: Boston, MA 02115

APPLICANT: Bunn, H. Franklin
APPLICANT: Wen, Danyi
APPLICANT: Showers, Mark O.
TITLE OF INVENTION: Erythropoietin Muteins With Enhanced
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION/DOCKET NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
TOPOLOGY: both
PCT-US94-04361-37

Query Match 97.9%; Score 851; DB 5; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.4e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APRLLCDSRVLYRLLYLLLEAKENITTCGAHCSLNENITVPTKYNFYAWKMEVGOQA 63
Db 1 APRLLCDSRVLYRLLYLLLEAKENITTCGAHCSLNENITVPTKYNFYAWKMEVGOQA 60
QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 123
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 124 PDASAAAPLRTITADTFKLFVYNSFLRGKLYTGEACRTGDR 169
Db 121 PDASAAAPLRTITADTFKLFVYNSFLRGKLYTGEACRTGDR 166

RESULT 6
US-07-903-220-1
Sequence 1, Application US/07903220
Patent No. 5322837
GENERAL INFORMATION:
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF
TITLE OF INVENTION: ERYTHROPOIETIN AND ERYTHROPOIETIN COMPOSITION
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul H. Heller
STREET: Kenyon & Kenyon, One Broadway
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10004
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,220
FILING DATE: 19920731
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION/DOCKET NUMBER: 32,724
REFERENCE/DOCKET NUMBER: 1248/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-07-903-220-1

Query Match 97.9%; Score 851; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 5.6e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APRLLCDSRVLYRLLYLLLEAKENITTCGAHCSLNENITVPTKYNFYAWKMEVGOQA 63
Db 28 APRLLCDSRVLYRLLYLLLEAKENITTCGAHCSLNENITVPTKYNFYAWKMEVGOQA 87
QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 123
Db 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 147
QY 124 PDASAAAPLRTITADTFKLFVYNSFLRGKLYTGEACRTGDR 169
Db 148 PDASAAAPLRTITADTFKLFVYNSFLRGKLYTGEACRTGDR 193

RESULT 7
US-08-883-795A-34
Sequence 34, Application US/08883795A
Patent No. 5985607
GENERAL INFORMATION:
APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-883-795A-34

Query Match          97.9%; Score 851; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 5.6e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 APPRLCDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVQQA 63
Db      28 APPRLCDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVQQA 87
QY      64 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 123
Db      88 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 147
QY      124 PPDAASAAPLRTITADTFRKLFVYSNLFRLGKLYTGEACRTGDR 169
Db      148 PPDAASAAPLRTITADTFRKLFVYSNLFRLGKLYTGEACRTGDR 193

RESULT 8
US-09-552-265B-4
; Sequence 4; Application US/09552265B
; Patent No. 6555343
; GENERAL INFORMATION:
; APPLICANT: DeSavage, Frederick
; APPLICANT: Hemmer, Dennis, J.
; TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
; TITLE OF INVENTION: polypeptides and nucleic acids encoding the same
; FILE REFERENCE: GENENT. 057CE1
; CURRENT APPLICATION NUMBER: US/09/552,265B
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: US 09/307307
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-552-265B-4

Query Match          97.9%; Score 851; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 5.6e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 APPRLCDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVQQA 63
Db      28 APPRLCDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVQQA 87
QY      64 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 123
Db      88 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 147
QY      124 PPDAASAAPLRTITADTFRKLFVYSNLFRLGKLYTGEACRTGDR 169
Db      148 PPDAASAAPLRTITADTFRKLFVYSNLFRLGKLYTGEACRTGDR 193

RESULT 9
US-09-366-009-34
; Sequence 34; Application US/09366009
; Patent No. 6426042
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; APPLICANT: Ueno, Takashi
; Uemori, Takashi
; Ueno, Takashi
; Koyama, No. 6426042uto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
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; US-09-366-009-34

Query Match          97.6%; Score 848; DB 4; Length 412;
Best Local Similarity 99.4%; Pred. No. 4.4e-97;
Matches 165; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 APPRLCDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVQQA 63
Db      233 APPRLCDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKMEVQQA 292
QY      64 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 123
Db      293 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLLRALGAQKEAIS 352
QY      124 PPDAASAAPLRTITADTFRKLFVYSNLFRLGKLYTGEACRTGDR 169
Db      353 PPDAASAAPLRTITADTFRKLFVYSNLFRLGKLYTGEACRTGDR 398

RESULT 10
US-08-809-156B-34
; Sequence 34; Application US/08809156B
; Patent No. 6472204
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; APPLICANT: Uemori, Takashi
; APPLICANT: Ueno, Takashi
```

APPLICANT: Koyama, No. 6472204uto
 APPLICANT: Hashino, Kimikazu
 APPLICANT: Kato, Ikunoshin
 TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
 TITLE OF INVENTION: CELLS WITH RETROVIRUS
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WEISER & ASSOCIATES
 STREET: 230 South Fifteenth Street, Suite 500
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/809,156B
 FILING DATE: 07-MAR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP96/03254
 FILING DATE: 07-NOV-1996
 APPLICATION DATA:
 APPLICATION NUMBER: JP 294382/1995
 FILING DATE: 13-NOV-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 051847/1996
 FILING DATE: 08-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Weiser, Gerard J.
 REGISTRATION NUMBER: 19,763
 REFERENCE/DOCKET NUMBER: 977.6507P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-875-8383
 TELEFAX: 215-875-8394
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 412 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-809-156B-34

Query Match 97.6%; Score 848; DB 4; Length 412;
 Best Local Similarity 99.4%; Pred. No. 4.4e-97;
 Matches 165; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKMEVGGQA 63
 Db 233 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKMEVGGQA 292
 QY 64 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 123
 Db 293 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 352
 QY 124 PDASAAPLRTITADTFRKLFVSNFLRGKLYTGEACRTGD 169
 Db 353 PDASAAPLRTITADTFRKLFVSNFLRGKLYTGEACRTGD 398

RESULT 11
 US-09-604-871-1
 ; Sequence 1, Application US/09604871
 ; Patent No. 6340742
 ; GENERAL INFORMATION:
 ; APPLICANT: Burg, Josef
 ; APPLICANT: Hilger, Bernd
 ; APPLICANT: Josel, Hans-Peter
 ; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES

; FILE REFERENCE: 1098 nonprovisional
 ; CURRENT APPLICATION NUMBER: US/09/604,871
 ; CURRENT FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/151,454
 ; PRIOR FILING DATE: 1999-08-30
 ; PRIOR APPLICATION NUMBER: 60/147,452
 ; PRIOR FILING DATE: 1999-08-05
 ; PRIOR APPLICATION NUMBER: 60/142,243
 ; PRIOR FILING DATE: 1999-07-02
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 165
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-604-871-1

Query Match 97.4%; Score 846; DB 3; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.8e-97;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKMEVGGQA 63
 Db 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKMEVGGQA 60
 QY 64 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 123
 Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 120
 QY 124 PDASAAPLRTITADTFRKLFVSNFLRGKLYTGEACRTGD 168
 Db 121 PDASAAPLRTITADTFRKLFVSNFLRGKLYTGEACRTGD 165

RESULT 12
 US-09-604-938-1
 ; Sequence 1, Application US/09604938
 ; Patent No. 6583272
 ; GENERAL INFORMATION:
 ; APPLICANT: Bailon, Pascal
 ; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
 ; FILE REFERENCE: 1097 nonprovisional
 ; CURRENT APPLICATION NUMBER: US/09/604,938
 ; CURRENT FILING DATE: 2000-06-27
 ; PRIOR APPLICATION NUMBER: 60/166,151
 ; PRIOR FILING DATE: 1999-11-17
 ; PRIOR APPLICATION NUMBER: 60/151,548
 ; PRIOR FILING DATE: 1999-08-13
 ; PRIOR APPLICATION NUMBER: 60/150,225
 ; PRIOR FILING DATE: 1999-08-23
 ; PRIOR APPLICATION NUMBER: 60/142,254
 ; PRIOR FILING DATE: 1999-07-02
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 165
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-604-938-1

Query Match 97.4%; Score 846; DB 4; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.8e-97;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKMEVGGQA 63
 Db 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKMEVGGQA 60
 QY 64 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 123
 Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 120
 QY 124 PDASAAPLRTITADTFRKLFVSNFLRGKLYTGEACRTGD 168

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OM protein - protein search, using sw model

Run on: November 19, 2004, 21:11:10 ; Search time 80.087 Seconds
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747.281 Million cell updates/sec

Title: US-10-014-363-4

Perfect score: 869

Sequence: 1 APPAPRLICDSRLVRLYL.....NFLRGKLYTGACRTGDR 169

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Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	856.5	98.6	174	13	US-10-014-363-5
4	851	97.9	166	9	US-09-853-731-2
5	851	97.9	166	13	US-10-014-363-2
6	851	97.9	166	14	US-10-241-356-2
7	851	97.9	166	14	US-10-293-551-2
8	851	97.9	166	14	US-10-400-377-2
9	851	97.9	166	14	US-10-400-708-2
10	851	97.9	166	14	US-10-298-148-2
11	851	97.9	166	15	US-10-360-101-227
12	851	97.9	166	15	US-10-467-115-1
13	851	97.9	166	16	US-10-658-834A-201

14	851	97.9	166	16	US-10-773-939-2	Sequence 2, Appli
15	851	97.9	166	16	US-10-774-149-2	Sequence 2, Appli
16	851	97.9	166	16	US-10-468-496-133	Sequence 133, App
17	851	97.9	166	17	US-10-773-654-2	Sequence 2, Appli
18	851	97.9	193	10	US-09-813-775C-4	Sequence 4, Appli
19	851	97.9	193	14	US-10-113-824-2	Sequence 2, Appli
20	851	97.9	193	16	US-10-612-665-10	Sequence 10, Appl
21	851	97.9	193	16	US-10-612-665-22	Sequence 22, Appl
22	851	97.9	193	16	US-10-612-665-112	Sequence 112, App
23	851	97.9	193	17	US-10-676-694-10	Sequence 10, Appl
24	851	97.9	193	17	US-10-676-694-22	Sequence 22, Appl
25	851	97.9	193	17	US-10-676-694-112	Sequence 112, App
26	851	97.9	428	14	US-10-435-608-10	Sequence 10, Appl
27	851	97.9	428	15	US-10-622-108-10	Sequence 10, Appl
28	849	97.7	166	16	US-10-658-834A-959	Sequence 959, App
29	849	97.7	166	16	US-10-658-834A-967	Sequence 967, App
30	848	97.6	166	16	US-10-658-834A-952	Sequence 952, App
31	848	97.6	166	16	US-10-658-834A-955	Sequence 955, App
32	848	97.6	166	16	US-10-658-834A-958	Sequence 958, App
33	848	97.6	166	16	US-10-658-834A-966	Sequence 4, Appli
34	848	97.6	193	14	US-10-435-608-4	Sequence 4, Appli
35	848	97.6	193	15	US-10-622-108-4	Sequence 63, Appl
36	848	97.6	193	16	US-10-612-665-63	Sequence 64, Appl
37	848	97.6	193	16	US-10-612-665-64	Sequence 70, Appl
38	848	97.6	193	16	US-10-612-665-70	Sequence 81, Appl
39	848	97.6	193	16	US-10-612-665-81	Sequence 88, Appl
40	848	97.6	193	16	US-10-612-665-88	Sequence 91, Appl
41	848	97.6	193	16	US-10-612-665-91	Sequence 63, Appl
42	848	97.6	193	17	US-10-676-694-63	Sequence 64, Appl
43	848	97.6	193	17	US-10-676-694-64	Sequence 70, Appl
44	848	97.6	193	17	US-10-676-694-70	Sequence 81, Appl
45	848	97.6	193	17	US-10-676-694-81	

ALIGNMENTS

RESULT 1
US-10-014-363-4
; Sequence 4, Application US/10014363
; Publication No. US20020115833A1
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 169
; TYPE: PRT
; ORGANISM: CHO/dhfr-
US-10-014-363-4

Query Match 100.0%; Score 869; DB 13; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.4e-86;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPAPRLICDSRLVRLYLLEAKEAENTTTCACHCNLNENITVPDTKVNFYAKRMEVG 60

Db 1 APPAPRLICDSRLVRLYLLEAKEAENTTTCACHCNLNENITVPDTKVNFYAKRMEVG 60

QY 61 QQAVEVWQGLALLSEAVLRGQALLVNSQPEPLQHVDKAVSGRLSLTTLRALGAOKE 120

Db 61 QQAVEVWQGLALLSEAVLRGQALLVNSQPEPLQHVDKAVSGRLSLTTLRALGAOKE 120

```

QY 121 AISPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGDR 169
DB 121 AISPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGDR 169

RESULT 2
US-10-014-363-3
; Sequence 3, Application US/10014363
; Publication No. US20020115833A1
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 174
; TYPE: PRT
; ORGANISM: CHO/dhfr-
US-10-014-363-3

Query Match 98.6%; Score 856.5; DB 13; Length 174;
Best Local Similarity 97.1%; Pred. No. 3.5e-85;
Matches 169; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 APP-----APRLICDSRVRLYLEAKEAENITTCGAHCSLNENITVPDTKVNFYAWK 55
DB 1 APPRIEGRAPRLICDSRVRLYLEAKEAENITTCGAHCSLNENITVPDTKVNFYAWK 60

QY 56 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKVGSLRSLTLLRAL 115
DB 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKVGSLRSLTLLRAL 120

QY 116 GAOKEAISPPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGDR 169
DB 121 GAOKEAISPPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGDR 174

RESULT 3
US-10-014-363-5
; Sequence 5, Application US/10014363
; Publication No. US20020115833A1
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 174
; TYPE: PRT
; ORGANISM: CHO/dhfr-
US-10-014-363-5

Query Match 98.6%; Score 856.5; DB 13; Length 174;
Best Local Similarity 97.1%; Pred. No. 3.5e-85;
Matches 169; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

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QY 1 APP-----APRLICDSRVRLYLEAKEAENITTCGAHCSLNENITVPDTKVNFYAWK 55
DB 1 APPGAHYAPRLICDSRVRLYLEAKEAENITTCGAHCSLNENITVPDTKVNFYAWK 60

QY 56 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKVGSLRSLTLLRAL 115
DB 61 RMEVGQAAVEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKVGSLRSLTLLRAL 120

QY 116 GAOKEAISPPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGDR 169
DB 121 GAOKEAISPPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGDR 174

RESULT 4
US-09-853-731-2
; Sequence 2, Application US/09853731
; Patent No. US20020037841A1
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/09/853,731
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-731-2

Query Match 97.9%; Score 851; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APRRLICDSRVRLYLEAKEAENITTCGAHCSLNENITVPDTKVNFYAWKMEVQQA 63
DB 1 APRRLICDSRVRLYLEAKEAENITTCGAHCSLNENITVPDTKVNFYAWKMEVQQA 60

QY 64 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKVGSLRSLTLLRALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKVGSLRSLTLLRALGAQKEAIS 120

QY 124 PDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGDR 169
DB 121 PDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGDR 166

RESULT 5
US-10-014-363-2
; Sequence 2, Application US/10014363
; Publication No. US20020115833A1
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-014-363-2

Query Match 97.9%; Score 851; DB 13; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGQQA 63
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGQQA 60
QY 64 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 124 PDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 169
DB 121 PDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 166

RESULT 6

US-10-241-356-2
; Sequence 2, Application US/10241356
; Publication No. US2003007753A1
; GENERAL INFORMATION:
; APPLICANT: TISCHER, WILHELM
; TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
; FILE REFERENCE: 20971
; CURRENT APPLICATION NUMBER: US/10/241,356
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: EP 01122555.4
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-241-356-2

Query Match 97.9%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGQQA 63
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGQQA 60
QY 64 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 124 PDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 169
DB 121 PDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 166

RESULT 7

US-10-293-551-2
; Sequence 2, Application US/10293551
; Publication No. US20030120045A1
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/10/293,551
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/09/604,938
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225

; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-551-2

Query Match 97.9%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGQQA 63
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGQQA 60
QY 64 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 124 PDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 169
DB 121 PDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 166

RESULT 8

US-10-400-377-2
; Sequence 2, Application US/10400377
; Publication No. US20030162949A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,377
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-377-2

Query Match 97.9%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGQQA 63
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVGQQA 60
QY 64 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 123
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 124 PDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 169
DB 121 PDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 166

RESULT 9

US-10-400-708-2
; Sequence 2, Application US/10400708
; Publication No. US20030166865A1
; GENERAL INFORMATION:

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; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,708
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-708-2

Query Match          97.9%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APRLLCDSRVRLRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVGGQA 63
Db 1 APRLLCDSRVRLRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVGGQA 60

QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 123
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 124 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYTGACRTGDR 169
Db 121 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYTGACRTGDR 166

RESULT 10
US-10-298-148-2
; Sequence 2, Application US/10298148
; Publication No. US20030171284A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/298,148
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-148-2

Query Match          97.9%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APRLLCDSRVRLRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVGGQA 63
Db 1 APRLLCDSRVRLRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVGGQA 60

QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 123
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 124 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYTGACRTGDR 169
Db 121 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYTGACRTGDR 166
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RESULT 11
US-10-360-101-227
; Sequence 227, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 227
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of erythropoietin
US-10-360-101-227

Query Match          97.9%; Score 851; DB 15; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APRLLCDSRVRLRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVGGQA 63
Db 1 APRLLCDSRVRLRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVGGQA 60

QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 123
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 124 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYTGACRTGDR 169
Db 121 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYTGACRTGDR 166

RESULT 12
US-10-467-115-1
; Sequence 1, Application US/10467115
; Publication No. US20040063917A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; TITLE OF INVENTION: MODIFIED ERYTHROPOIETIN (EPO) WITH
; FILE REFERENCE: MER-114
; CURRENT APPLICATION NUMBER: US/10/467,115
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: 01102615.0
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01174
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-467-115-1

Query Match          97.9%; Score 851; DB 15; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 14
US-10-773-939-2
; Sequence 2, Application US/10773939
; Publication No. US20040175356A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-1-PUS
; CURRENT APPLICATION NUMBER: US/10/773,939
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/10/400,377

	Query Match	97.9%;	Score 851;	DB 16;	Length 166;
	Best Local Similarity	100.0%;	Pred. No. 1.3e-84;		
	Matches 166;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	4	APPRLICDSRVLERYLLLEAKEAENITTTGCAEHCSLNENITVPDTKYNFYAWKMEVGGQA	63		
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QY	64	VEVWQGLALLSVAVLRGQALLVNSQPWEPLQIHDVKAVSGLSRLTTTLRALGAQKEAIS	123		
Db	61	VEVWQGLALLSVAVLRGQALLVNSQPWEPLQIHDVKAVSGLSRLTTTLRALGAQKEAIS	120		
QY	124	PPDAASAAPLRTITADTFRKLFRVYSNFIURGKLKIYTGACRTGDR	169		
Db	121	PPDAASAAPLRTITADTFRKLFRVYSNFIURGKLKIYTGACRTGDR	166		

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Job time : 81.087 secs

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OM protein - protein search, using sw model

Run on: November 19, 2004, 20:59:24 ; Search time 19.6132 Seconds
(without alignments)
829.068 Million cell updates/sec

Title: US-10-014-363-4

Perfect score: 869

Sequence: 1 APPAPRLICDSRVRLRYLL.....NFLRGKLYTGACRTGDR 169

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	97.9	193	1 ZUHU	erythropoietin pre
2	774.5	89.1	192	1 JQ0173	erythropoietin pre
3	769.5	88.6	192	1 I84613	erythropoietin pre
4	718	82.6	188	1 I46083	erythropoietin pre
5	706	81.2	192	1 S28148	erythropoietin pre
6	690.5	79.5	194	1 I46401	erythropoietin pre
7	686	78.9	192	1 A24902	erythropoietin pre
8	685.5	78.9	195	2 JC7699	erythropoietin pre
9	683	78.6	190	2 I46578	erythropoietin - r
10	638	73.4	175	2 I46199	erythropoietin - p
11	97	11.2	353	2 G02729	erythropoietin - d
12	96	11.0	353	2 I80105	erythropoietin - h
13	93	10.7	286	2 A55530	thrombopoietin pre
14	88	10.1	323	2 AB0323	megakaryocyte grow
15	87.5	10.1	346	2 AB0959	ribonucleoside-dip
16	85	9.8	339	2 A83274	Solute binding rec
17	83.5	9.6	296	2 AI0443	UDP-N-acetylpyruvo
18	83.5	9.6	480	2 S56639	probable 2-hydroxy
19	81	9.3	326	2 JC1125	ribosomal protein
20	80.5	9.3	3033	1 GNNWJ8	thrombopoietin pre
21	79.5	9.1	1829	2 T35681	genome polyprotein
22	78.5	9.0	813	2 AF0526	probable sensory h
23	78.5	9.0	897	2 A54696	ATP-dependent heli
24	78	9.0	348	2 T35450	EGF receptor subut
25	78	9.0	455	2 AG2919	ABC transporter AT
26	78	9.0	455	2 H97693	conserved hypothet
27	78	9.0	747	1 S36741	methylamine utiliz
28	77.5	8.9	242	2 AD1928	probable copper-tr
29	77	8.9	451	2 S75569	hypothetical prote

ALIGNMENTS

RESULT 1

ZUHU

erythropoietin precursor [validated] - human

C;Species: Homo sapiens (man)

C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004

C;Accession: A01855; A24744; A25384; A22210; S56178

R;Jacobs, K.; Shoemaker, C.; Rudersdorf, R.; Neill, S.D.; Kaufman, R.J.; Mufson, A.; See Nature 313, 806-810, 1985

A;Title: Isolation and characterization of genomic and cDNA clones of human erythropoiet

A;Reference number: A01855; MUID:85137899; PMID:3838366

A;Accession: A01855

A;Molecule type: mRNA; DNA

A;Residues: 1-193 <JAC>

A;Cross-references: UNIPROT:P01588; GB:X02157; GB:X02158

R;Lin, F.K.; Suggs, S.; Lin, C.H.; Browne, J.K.; Smalling, R.; Egrie, J.C.; Chen, K.K.; Proc. Natl. Acad. Sci. U.S.A. 82, 7580-7584, 1985

A;Title: Cloning and expression of the human erythropoietin gene.

A;Reference number: A24744; MUID:86067948; PMID:3865178

A;Accession: A24744

A;Molecule type: DNA

A;Residues: 1-193 <LIN>

A;Cross-references: GB:M11319; NID:g182197; PIDN:AAAS2400.1; PID:g182198

R;Lai, P.H.; Everett, R.; Wang, F.F.; Arakawa, T.; Goldwasser, E. J. Biol. Chem. 261, 3116-3121, 1986

A;Title: Structural characterization of human erythropoietin.

A;Reference number: A25384; MUID:86140080; PMID:3949763

A;Accession: A25384

A;Molecule type: protein

A;Residues: 28-86, 'Q', 87-193 <LAI>

A;Experimental source: urine

A;Note: forms without the carboxyl-terminal residue and the four carboxyl-terminal resid

R;Yanagawa, S.; Hixade, K.; Ohnata, H.; Sasaki, R.; Chiba, H.; Ueda, M.; Goto, M. J. Biol. Chem. 259, 2707-2710, 1984

A;Title: Isolation of human erythropoietin with monoclonal antibodies.

A;Reference number: A22210; MUID:84135751; PMID:6698989

A;Accession: A22210

A;Molecule type: protein

A;Residues: 28-29, 'X', 31-33, 'L', 35-50, 'X', 52-53, 'D', 55, 'G', 57 <YAN>

R;Matsumoto, S.; Ikura, K.; Ueda, M.; Sasaki, R. Plant Mol. Biol. 27, 1163-1172, 1995

A;Title: Characterization of a human glycoprotein (erythropoietin) produced in cultured

A;Reference number: S56178; MUID:95284365; PMID:7766897

A;Accession: S56178

A;Molecule type: protein

A;Residues: 28-33, 'X', 35-37 <MTS>

C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o

C;Genetics:

A;Gene: GDB:EPO

A;Cross-references: GDB:119110; OMIM:133170

A;Map position: 7q21.3-7q22.1

A;Introns: 5/1; 53/3; 82/3; 142/3

C;Function:

A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; Glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-193/Product: erythropoietin #status experimental <MAT>
F;34-188,56-60/Disulfide bonds: #status experimental
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;153/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 97.9%; Score 851; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.8e-73;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 63
DB 28 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 87

QY 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 123
DB 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 147

QY 124 PDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 169
DB 148 PDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 193

RESULT 2
JQ0173
erythropoietin precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 07-Sep-1990 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: JQ0173
R;Lin, F.K.; Lin, C.H.; Lai, P.H.; Browne, J.K.; Egrie, J.C.; Smalling, R.; Fox, G.M.; Q
Gene 44, 201-209, 1986
A;Title: Monkey erythropoietin gene: cloning, expression and comparison with the human e
A;Reference number: JQ0173; MUID:87055236; PMID:2877922
A;Accession: JQ0173
A;Molecule type: mRNA
A;Residues: 1-192 <LIN>
A;Cross-references: UNIPROT:P07865; GB:M18189; GB:M15819; GB:M18188; NID:g342
A;Experimental source: kidney
C;Comment: This protein is the principal hormone involved in the regulation of erythrocy
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function:
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; Glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 89.1%; Score 774.5; DB 1; Length 192;
Best Local Similarity 91.1%; Pred. No. 5e-66;
Matches 153; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 2 PPAPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQ 61
DB 26 PGAPRLICDSRVLYRYLLEAKEAENITTCGSCSCLNENITVPDTKVFYAKRMEVGQ 85

QY 62 QAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEA 121
DB 86 QAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQ-EA 144

QY 122 ISPPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 169
DB 145 ISLPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 192

RESULT 3
184613
erythropoietin precursor - rhesus macaque

C;Species: Macaca mulatta (rhesus macaque)
C;Date: 02-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: I84613
R;Men, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I84613
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-192 <RES>
A;Cross-references: UNIPROT:Q28513; GB:I10609; NID:g342095; PIDN:AAA36842.1; PID:g342096
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function:
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; Glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 88.6%; Score 769.5; DB 1; Length 192;
Best Local Similarity 89.9%; Pred. No. 1.5e-65;
Matches 151; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 2 PPAPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQ 61
DB 26 PGAPRLICDSRVLYRYLLEAKEAENITTCGSCSCLNENITVPDTKVFYAKRMEVGQ 85

QY 62 QAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEA 121
DB 86 QAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQ-EA 144

QY 122 ISPPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 169
DB 145 ISLPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 192

RESULT 4
I46083
erythropoietin precursor - cat (fragment)
C;Species: Felis silvestris catus (domestic cat)
C;Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: I46083
R;Men, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I46083
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-188 <WEN>
A;Cross-references: UNIPROT:P33708; GB:I10606; NID:g163820; PIDN:AAA30807.1; PID:g16382
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function:
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; Glycoprotein; hormone; kidney; liver
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-188/Product: erythropoietin #status predicted <MAT>
F;29-183,51-55/Disulfide bonds: #status predicted
F;46,60,105/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 82.6%; Score 718; DB 1; Length 188;
Best Local Similarity 84.3%; Pred. No. 1.1e-60;
Matches 140; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 4 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 63
DB 23 APPRLICDSRVLYRYLLEAKEAENITTCGSCSCLNENITVPDTKVFYAKRMEVGQQA 82

[illegible]

RESULT 5
S28148 erythropoietin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: S28148; I62743
R;Nagao, M.; Suga, H.; Okano, M.; Maeuda, S.; Narita, H.; Ikura, K.; Sasaki, R.
Biochim. Biophys. Acta 1171, 99-102, 1992
A;Title: Nucleotide sequence of rat erythropoietin.
A;Reference number: S28148; MUID:93042015; PMID:1420369
A;Accession: S28148
A;Molecule type: mRNA
A;Residues: 1-192 <NAG>
A;Cross-references: UNIPROT:P29676; GB:D10763; NID:G220735; PIDN:BAA01593.1; PID:G220736
R;Men, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homology
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I62743
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 4-192 <RES>
A;Cross-references: GB:I10608; NID:G204060; PIDN:BAA41126.1; PID:G204061
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver c
C;Function:
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-192/Product: erythropoietin #status predicted <MAT>
F;33-187,55-165/Diulfide bonds: #status predicted
F;50,64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	81.2%	Score 706;	DB 1;	Length 192;
Best Local Similarity	82.5%;	Pred. No. 1.6e-59;		
Matches 137;	Conservative 13;	Mismatches 16;	Indels 0;	Gaps 0;
QY	4	APRLLICDSRLVRYLLEAKEAENITTCGAEHCSLNENITVPDTKVNIFYAKRWVEVQQA	63	
Db				
QY	27	APRLLICDSRLVRYLLEAKEAENVTCGAEGRPSENITVPDTKVNIFYAKRWKVEQA	86	
Db				
QY	64	VEVWQGLALLSEAVLRGQALLVNSQSPWEPLQLHVDKAVSGRLSLTLLRLAIGKAQKEAIS	123	
Db				
QY	87	VEVWQGLSLLSEAILQAQALQANSQSPPEISQLHIDKAI SGLRSLTSLRLVIGKAQKELMS	146	
Db				
QY	124	PPDAASAAPLRTITADTFRKLFVRVYSNFLRGKMLKLYTGEACRTGDR	169	
Db				
QY	147	PPDATAAPLRTITADTFCFLFRVYSNFLRGKMLKLYTGEACRTGDR	192	
Db				

RESULT 6
I46401
erythropoietin precursor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C:Accession: I46401; I47077
R:Fu, P.; Evans, B.; Lim, G.B.; Moritz, K.; Wintour, E.M.
Mol. Cell. Endocrinol. 93, 107-116, 1993
A:Title: The sheep erythropoietin gene: molecular cloning and effect of hemorrhage on pl
A:Reference number: I46401; MUID:93351736; PMID:8349021
A:Accession: I46401
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A;Residues: 1-194 <FUX>
A;Cross-references: UNIPROT:P33709; EMBL:Z24681; NID:g395049; PIDN:CAA80848.1; PID:g395049; Men, D.; Boissel, J.
Blood 32, 1507-1516, 1993
A;Title: erythropoietin structure-function relationships: High degree of sequence homology between human and mouse erythropoietin
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I47077
A;Status: translated from GB/EMBL/DBBJ
A;Molecule type: mRNA
A;Residues: 4-15, 'L', 17-107, 'P', 109-194 <WEN>
A;Cross-references: GB:II0610; NID:gl65876; PIDN:AAA31518.1; PID:gl65877
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver & placenta of fetal mammals
C;Function:
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIO>
F;28-194/Product: erythropoietin #status predicted <WAT>
F;34-189,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carboxylate (Asn) (covalent) #status predicted
F;154/Binding site: carboxylate (Ser) (covalent) #status predicted

Query Match	79.5%	Score 690.5	DB 1	Length 194
Best Local Similarity	82.0%	Pred. No. 4.6e-58		
Matches 137	Conservative	9	Mismatches 20	Indels 1
QY	4	APPRLLCDSVLERYLLEAKAEENITTCGAHCHSLNENITVPDTKUNFYAKRWVEVQQA	63	
Db				
	28	APPRLLCDSVLERYLLEAKAEENATMGCAEGCSFSENITVPDTKUNFYAKRWVEVQQA	87	
QY	64	VEYWGQGLALLSEAVLRGQALLVNSQWPEPLQLHLVDKAVSGLSRLTLLRALGAKQKAIS	123	
Db	88	LEVWQGLALLSEALFRGQALLANASQPCREALRLHVDKAVSGLSRLTSLRALGAKQKAIP	147	
QY	124	PPDAA-SAAPLRTITADTFKRLPRVYSNFIURGKKLYTGACACRGDR	169	
Db	148	LPDATSAAPLRTFTVDALSKLFRIYSNFIURGKKLYTGACACRGDR	194	

RESULT 7
A24902 erythropoietin precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Oct-1987 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C:Accession: A24902; A24901
R:Shoemaker, C.B.; Mitsock, L.D.
Mol. Cell. Biol. 6, 849-858, 1986
A:Title: Murine erythropoietin gene: cloning, expression, and human gene homology.
A:Reference number: A24902; PMID:87039105; PMID:3773894
A:Accession: A24902
A:Molecule type: DNA
A:Residues: 1-192 <SHO>
A:Cross-references: UNIPROT:P07321
A:Note: the authors translated the codon TTA for residue 12 as Phe, TTA for residue 43 a
R:McDonald, J.D.; Lin, F.K.; Goldwasser, E.
Mol. Cell. Biol. 6, 842-848, 1986
A:Title: Cloning, sequencing, and evolutionary analysis of the mouse erythropoietin gene
A:Reference number: A24901; PMID:87039104; PMID:3022133

A:Accession type: DNA
A:Residues: 1-67, 'p', 69-192 <MCD>
A:Cross-references: GB:M12930; NID:gl93086; PIDN:AAA37570.1; PID:g387152
C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of
C:Genetics:
A:Introns: 5/1; 52/3; 81/3; 141/3
C:Function:
A:Description: the primary inducer of erythrocyte formation
C:Superfamily: erythropoietin
C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-192/Product: erythropoietin #status predicted <MAT>
F:33-187,55-165/Dissulfide bonds: #status predicted
F:50,64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	78.6%;	Score 683;	DB 2;	Length 190;
Best Local Similarity	82.1%;	Pred: No. 2.3e-57;		
Matches 138; Conservative	7;	Mismatches 21;	Indels	2; Gaps 1;
QY	4	APPRLICDSRVLYRLLBAKAENITTTGCAECSLNNETVPDTKVFNFAWRMEVGQQA	63	
DBB	23	APPRLICDSRVLYRLLBAKGENATMGAESCSPSENITVPDTKVFNFAWRMEVGQQA	82	
QY	64	VVEWQGLALLGEAVLRGQALLVNNSQPWEPLQHVDKAVSGRLSRTTLRALGAQKEAIS	123	
DBB	83	MEVWQGLALLSEAILQQGALLANSQPSGALQHVVDKAVSGRLSRTSLLRALGAQKEAIP	142	
QY	124	PPDA--ASAAPLTITATFTFKLVFVYSNFLRGKLKYTGACRTGDR	169	
DBB	143	LFDASPSSATPLTRTFAVDTCLCKLFNYSNFLRGKUTLYTGACRRRDD	190	

```

RESULT 10
I46199
erythropoietin - dog (fragment)
C.Species: Canis lupus familiaris (dog)
C.Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C.Accession: I46199
R.Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A.Title: Erythropoietin structure-function relationships: High degree of sequence conservation
A.Reference number: I46083; MUID:93372347; PMID:8364201
A.Accession: I46199
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-175 <MEN>
A.Cross-references: UNIPROT:P33707; GB:I13027; PIDN:AAA30842.1; PI
C.Superfamily: erythropoietin

Query Match 73.4%; Score 638; DB 2: Length 175;
Best Local Similarity 81.0%; Pred. NO. 3.9e-53;
Matches 124; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

```

23	APRPLICDSRVLERVILEAREAVNTMGCAQGSFSENITVPTKYNFYTWKMDVGGQA	82
64	VEVWQGLALLSEAVLRGQALLVNSQPWEPLQIHDVKAVSGLSRLTTLRALGAQKEAIS	123
83	LEVWQGLALLSEAILRGQALLANASQFETPOLHVDKAVSSLRSLTSLLRALGAQKEAMS	142
124	PPDAASAPLRTITADTFPRKLFPRVYSNFLRGKL	156
143	LPEEASAPLRTFTFTDLCFLPRIYSNFLRGKL	175
RESULT 11		
G02729		
thrombopoietin - human		

C:Accession: G02729
 R:im, S.
 submitted to the EMBL Data Library, May 1996
 A:Reference number: H01637
 A:Accession: G02729
 A:Status: preliminary; translated from GB/EMBL/DDRU
 A:Molecule type: mRNA
 A:Residues: 1-353 rIMX>
 A:Cross-references: EMBL:U59493; NID:g1401245; PIDN:AAB03392.1; PID:g1401246
 C:Genetics:
 A:Gene: rIPO
 Query Match 11.2%; Score 97; DB 2; Length 353;
 Best Local Similarity 26.8%; Pred. No. 0.18;
 Matches 42; Conservative 20; Mismatches 75; Indels 20; Gaps 5

A;Cross-references: GDB:374007; OMIM:600044
A;Map position: 3q26.3-3q27
A;Introns: 5/1; 47/3; 76/3; 132/3
C;Keywords: alternative splicing; cytokine; glycoprotein

Query Match 11.0%; Score 96; DB 2; Length 353;
Best Local Similarity 26.8%; Pred. No. 0.22;
Matches 42; Conservative 20; Mismatches 75; Indels

Qy 3 PAPPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNFT
 ||||| : : : : : : : : : : : : : : : : : :
Db 23 PAPP--ACDLRVLSKLRRSHVLSLSCQPEVHPPLTPFVLLPAVDPSL
 ||||| : : : : : : : : : : : : : : : : : :
Qy 63 AVEVWQGLALLSEAVL--RGQALLVNSSQPWEPLQLHVDKAVSGSLRT
 :: : : : : : : : : : : : : : : : : :
Db 81 AQDILGAVTLLEGVMAARGQLGPTCLSSLLGQLSGQVRLLIGALQSL-
 : : : : : : : : : : : : : : : : : :
Qy 121 AISPPDAASAAPLRITATDFKLFVYSNFLRGKLGK 157
 ||||| : : : : : : : : : : : : : : : : : :
Db 133 --LPQG-----RTAHKDPNAIFLSFOHLLRGKVR 161
 ||||| : : : : : : : : : : : : : : : : : :

RESULT 13
A55530
megakaryocyte growth and development factor, long form - human
N;Alternate names: MPL ligand, long form
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
C;Accession: A55530
R;Chang, M.; McNinch, J.; Basu, R.; Shutter, J.; Hsu, R.; Perkin
J. Biol. Chem. 270, 511-514, 1995
A;Title: Cloning and characterization of the human megakaryocyt
A;Reference number: A55530; MUID:95122483; PMID:7822271
A;Accession: A55530
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-286 <CHA>
A;Cross-references: GB:UI7071
C;Genetics:
A;Gene: MGDF
A;Map position: 3q26.3
C;Keywords: alternative splicing; cytokine

Query Match 10.7%; Score 93; DB 2; Length 286;
Best Local Similarity 27.1%; Pred. No. 0.33;
Matches 42; Conservative 18; Mismatches 75; Indels

Qy 3 PAPPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNFT
 ||||| : : : : : : : : : : : : : : : : : :
Db 23 PAPP--ACDLRVLSKLRRSHVLSLSCQPEVHPPLTPFVLLPAVDPSLC
 ||||| : : : : : : : : : : : : : : : : : :
Qy 63 AVEVWQGLALLSEAVL--RGQALLVNSSQPWEPLQLHVDKAVSGSLRT
 :: : : : : : : : : : : : : : : : : :
Db 81 AQDILGAVTLLEGVMAARGQLGPTCLSSLLGQLSGQVRLLIGALQSL-
 : : : : : : : : : : : : : : : : : :
Qy 121 AISPPDAASAAPLRITATDFKLFVYSNFLRGK 155
 ||||| : : : : : : : : : : : : : : : : : :
Db 133 --LPQG-----RTAHKDPNAIFLSFOHLLRGK 159
 ||||| : : : : : : : : : : : : : : : : : :

RESULT 14
AB0323
ribonucleoside-diphosphate reductase (EC 1.17.4.1) beta chain [il
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change
C;Accession: AB0323
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holder
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0323

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 20:59:03 ; Search time 101.008 Seconds
(without alignments)
962.682 Million cell updates/sec

Title: US-10-014-363-4

Perfect score: 869

Sequence: 1 APPAPRLICDSRLVRYLL.....NFLRGKLYTGACRTGDR 169

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	97.9	193	1	EPO HUMAN
2	851	97.9	193	2	AAP22357
3	774.5	89.1	192	1	EPO MACFA
4	769.5	88.6	192	1	EPO MACMU
5	728.5	83.8	192	2	Q867B1
6	711	81.2	192	1	EPO FELCA
7	706	81.2	192	1	EPO RAT
8	698	80.3	206	2	Q6PWU5
9	698	80.3	206	2	AAS77874
10	697.5	80.3	192	1	EPO BOVIN
11	694	79.9	192	1	EPO MOUSE
12	690.5	79.5	194	1	EPO SHEEP
13	685.5	78.9	195	2	Q9GKA2
14	685.5	78.9	195	2	Q9GKA3
15	683	78.6	190	1	EPO PIG
16	683	78.6	192	2	Q6H8S9
17	683	78.6	192	2	Q6H8T0
18	683	78.6	192	2	Q6H8T1
19	683	78.6	194	2	Q9MYM8
20	679	78.1	192	2	Q6H8T2
21	663	76.3	133	2	Q8H288
22	658	75.7	133	2	Q8H289
23	638	73.4	175	1	EPO CANFA
24	627	72.2	131	2	Q8H287
25	607	69.9	133	2	Q8H286
26	554	63.8	133	2	Q8H285
27	248	28.5	195	2	Q6UAM1
28	248	28.5	195	2	AAR25698
29	245	28.2	182	2	Q6JV23
30	245	28.2	182	2	AAQ72466
31	245	28.2	185	2	Q6JV22

32	245	28.2	185	2	AAQ72467
33	188	21.6	50	2	Q9QV40
34	116	13.3	352	1	TPO CANFA
35	115	13.2	177	2	Q6IYE9
36	96	11.0	353	1	TPO HUMAN
37	89.5	10.3	558	2	Q7ZUK7
38	88	10.1	323	2	Q8ZDC8
39	88	10.1	323	2	AAS62651
40	87.5	10.1	346	2	Q8Z2M5
41	87.5	10.1	346	2	Q8ZKZ4
42	87.5	10.1	432	2	Q7QDZ2
43	85	9.8	339	1	MURB PSEAE
44	85	9.8	3722	2	P94873
45	83.5	9.6	296	2	Q8ZAY4

ALIGNMENTS

RESULT 1
EPO_HUMAN

ID EPO_HUMAN STANDARD; PRT; 193 AA.

AC P01588; Q9UDZ0; Q9UEZ5; Q9UHA0;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Erythropoietin precursor (Epoetin).

GN Name=EPO;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85137899; PubMed=3838366;

RA Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J.,

RA Mufson A., Seehra J., Jones S.S., Hewick K., Fritsch E.F.,

RA Kawakita M., Shimizu T., Miyake T.,

RT "Isolation and characterization of genomic and cDNA clones of human

RT erythropoietin."

RL Nature 313:806-810(1985).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=86067948; PubMed=3865178;

RA Lin F.-K., Suggs S., Lin C.-H., Browne J.K., Smalling R., Egrie J.C.,

RA Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai P.-H.,

RA Goldwasser E.;

RT "Cloning and expression of the human erythropoietin gene."

RL Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=99018118; PubMed=9799793;

RA Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,

RA Tsui L.-C., Rosenthal A.;

RT "Large-scale sequencing of two regions in human chromosome 7q22:

RT analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci

RT reveals 17 genes."

RL Genome Res. 8:1060-1073(1998).

RN [4]

RP SEQUENCE FROM N.A.

RA Rupert J.L., Hochachka P.W.;

RT "Erythropoietin gene sequence in the Quechua, a high altitude native

RT population."

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE OF 58-193 FROM N.A., AND VARIANTS HEPATOCELLULAR CARCINOMA

RP 131-ASN-PHB-132 AND GIN-149.

RX MEDLINE=93384593; PubMed=8396923;

RA Funakoshi A., Muta H., Baba T., Shimizu S.;

RT "Gene expression of mutant erythropoietin in hepatocellular

RT carcinoma."

RL Biochem. Biophys. Res. Commun. 195:717-722(1993).

RN [6]

RP SEQUENCE OF 28-193, AND DISULFIDE BONDS.
RC TISSUE=urine;
RX MEDLINE=86140080; PubMed=3949763;
RA Lai P.H., Everett R., Wang F.F., Arakawa T., Goldwasser E.;
RT "Structural characterization of human erythropoietin.";
RL J. Biol. Chem. 261:3116-3121(1986).
RN [7]
RP PRELIMINARY SEQUENCE OF 28-57.
RX MEDLINE=84135751; PubMed=6698989;
RA Yanagawa S., Hirade K., Ohnata H., Sasaki R., Chiba H., Ueda M.,
RT Goto M.;
RT "Isolation of human erythropoietin with monoclonal antibodies.";
RL J. Biol. Chem. 259:2707-2710(1984).
RN [8]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=88153657; PubMed=3346214;
RA Takeuchi M., Takasaki S., Miyazaki H., Kato T., Hoshi S., Kochibe N.,
RT Kobata A.;
RT "Comparative study of the asparagine-linked sugar chains of human
erythropoietins purified from urine and the culture medium of
recombinant Chinese hamster ovary cells.";
RL J. Biol. Chem. 263:3657-3663(1988).
RN [9]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=89118279; PubMed=3219367;
RA Sasaki H., Ochi N., Dell A., Fukuda M.;
RT "Site-specific glycosylation of human recombinant erythropoietin:
analysis of glycopeptides or peptides at each glycosylation site by
fast atom bombardment mass spectrometry.";
RL Biochemistry 27:8618-8626(1988).
RN [10]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=92314463; PubMed=1820196;
RA Takeuchi M., Kobata A.;
RT "Structures and functional roles of the sugar chains of human
erythropoietins.";
RL Glycobiology 1:337-346(1991).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=98445092; PubMed=9774108; DOI=10.1038/26773;
RA Syed R.S., Reid S.W., Li C., Cheatham J.C., Aoki K.H., Liu B.,
RT Zhan H., Osslund T.D., Chirino A.J., Zhang J., Finer-Moore J.,
RA Elliott S., Siney K., Katz B.A., Matthews D.J., Wendoloski J.J.,
RA Egrie J., Stroud R.M.;
RT "Efficiency of signalling through cytokine receptors depends
critically on receptor orientation.";
RL Nature 395:511-516(1998).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
regulation of erythrocyte differentiation and the maintenance of a
physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
and by liver of fetal or neonatal mammals.
CC -!- PHARMACEUTICAL: Used for the treatment of anemia. Available under
the names Epogen (Amgen), Epogin (Chugai), Epomax (Elanex), Eprex
(Janssen-Cilag), Neorecormon or Recormon (Roche), and Procrit
(Ortho Biotech). Variations in the glycosylation pattern of EPO
distinguishes these products. Epogen, Epogin, Eprex and Procrit
are generically known as epoetin alfa, Neorecormon and Recormon as
epoetin beta and Epomax as epoetin omega.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
CC -!- DATABASE: NAME-R&D Systems' cytokine source book; EPO;
WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=197".
CC -----
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CC -----
CC EMBL; X02158; CAA26095.1; --

DR EMBL; X02157; CAA26094.1; --
DR EMBL; M11319; AA52400.1; --
DR EMBL; AF053356; AAC78791.1; --
DR EMBL; AF202308; AAF23132.1; --
DR EMBL; AF202306; AAF23132.1; JOINED.
DR EMBL; AF202307; AAF23132.1; JOINED.
DR EMBL; AF202310; AAF23133.1; --
DR EMBL; AF202309; AAF23133.1; JOINED.
DR EMBL; AF202311; AAF17572.1; --
DR EMBL; AF202314; AAF23134.1; --
DR EMBL; AF202312; AAF23134.1; JOINED.
DR EMBL; AF202313; AAF23134.1; JOINED.
DR EMBL; S65458; AAD13964.1; --
DR PIR; A01855; ZUHU.
DR PDB; 1BUY; NMR; A=28-193.
DR PDB; 1CN4; X-ray; C=28-193.
DR PDB; 1EER; X-ray; A=28-193.
DR GlycoSuiteDB; P01588; --
DR Genew; HGNC:3415; EPO.
DR MIM; 133170; --
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0006950; P:response to stress; TAS.
DR InterPro; IPR001323; EPO TPO.
DR InterPro; IPR003013; Erythroptn.
DR PIRSF; PIRSF001951; EPO; 1.
DR PRINTS; PRO0272; ERYTHROPTN.
DR PROSITE; PS00817; EPO TPO; 1.
KW 3D-structure; Direct protein sequencing; Erythrocyte maturation;
KW Glycoprotein; Hormone; Pharmaceutical; Polymorphism; Signal.
FT SIGNAL 1 27 Erythropoietin.
FT CHAIN 28 193 Removed in mature form (Probable).
FT PROPEP 190 193
FT DISULFID 34 188
FT DISULFID 56 60
FT CARBOHYD 51 51 N-linked (GlcNAc...).
FT CARBOHYD 65 65 /FTID=CAR_000052.
FT CARBOHYD 110 110 N-linked (GlcNAc...).
FT CARBOHYD 153 153 /FTID=CAR_000166.
FT CARBOHYD 153 153 /FTID=CAR_000192.
FT VARIANT 131 132 O-linked (GalNAc...).
FT SL -> NF (in an hepatocellular carcinoma).
FT /FTID=VAR_009870.
FT P -> Q (in an hepatocellular carcinoma).
FT /FTID=VAR_009871.
FT E -> Q (in Ref. 1; CAA26095).
FT Q -> QO (in Ref. 5).
FT G -> R (in Ref. 1; CAA26095).
FT CONFLICT 40 40
FT CONFLICT 85 85
FT CONFLICT 140 140
FT HELIX 32 34
FT HELIX 36 52
FT HELIX 53 55
FT TURN 57 58
FT STRAND 61 68
FT STRAND 73 73
FT HELIX 75 78
FT TURN 79 80
FT HELIX 83 109
FT HELIX 118 138
FT TURN 139 140
FT HELIX 141 147
FT TURN 148 149
FT STRAND 160 164
FT HELIX 165 177
FT TURN 178 178
FT HELIX 179 188
SQ SEQUENCE 193 AA; 21306 MW; C91F0E4C26A52033 CRC64;
Query Match 97.9%; Score 851; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.3e-71;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APRRLICDSRVLYRLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 63
 DB 28 APRRLICDSRVLYRLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 87
 QY 64 VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGRLSLTTLRALGAQKEAIS 123
 DB 88 VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGRLSLTTLRALGAQKEAIS 147
 QY 124 PPDAAASAPLRTITADTFKRLFRVYSNFKLGLKLYTGEACRTGDR 169
 DB 148 PPDAAASAPLRTITADTFKRLFRVYSNFKLGLKLYTGEACRTGDR 193

RESULT 2

AAP22357 PRELIMINARY; PRT; 193 AA.
 ID AAP22357
 AC AAP22357;
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
 DE Hypothetical protein EPO.
 GN EPO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99063792; PubMed=9847074;
 RA Wilson R.;
 RT "Toward a complete human genome sequence.";
 RL Genome Res. 8:1097-1108(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Doebber A., Elliott G., Jones T., Nguyen C., Stoneking T., Sun H.;
 RT "The sequence of Homo sapiens BAC clone RP11-336D7.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.H.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 KW EMBL; AC009488; AAP22357.1; --
 SQ SEQUENCE 193 AA; 21307 MW; C91F0E4C26A52033 CRC64;

Query Match 97.9%; Score 851; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1.3e-71;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 APRRLICDSRVLYRLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 63
 DB 28 APRRLICDSRVLYRLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 87
 QY 64 VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGRLSLTTLRALGAQKEAIS 123
 DB 88 VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGRLSLTTLRALGAQKEAIS 147
 QY 124 PPDAAASAPLRTITADTFKRLFRVYSNFKLGLKLYTGEACRTGDR 169
 DB 148 PPDAAASAPLRTITADTFKRLFRVYSNFKLGLKLYTGEACRTGDR 193

RESULT 3

EPO_MACFA

ID AC EPO_MACFA STANDARD; PRT; 192 AA.
 DT P07865;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=EPO;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8705236; PubMed=2877922;
 RA Lin F.-K., Lin C.-H., Lai P.-H., Browne J.K., Egrie J.C., Smalling R.,
 RA Fox G.M., Chen K.K., Castro M., Suggs S.;
 RT "Monkey erythropoietin gene: cloning, expression and comparison with
 the human erythropoietin gene.";
 RL Gene 44:201-209(1986).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 regulation of erythrocyte differentiation and the maintenance of a
 physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
 CC
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 CC
 CC EMBL; M8189; AAA36841.1; --
 DR PIR; JQ0173; JQ0173.
 DR HSSP; P01588; ICN4.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR001323; EPO_TPO_
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR FIRSF; FIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 192
 FT DISULFID 34 187
 FT DISULFID 56 60
 FT CARBOHYD 51 51
 FT CARBOHYD 65 65
 FT CARBOHYD 110 110
 FT CARBOHYD 152 152
 FT CARBOHYD 152 152
 SQ SEQUENCE 192 AA; 21113 MW; E8A900F42AD4522 CRC64;

Query Match 89.1%; Score 774.5; DB 1; Length 192;
 Best Local Similarity 91.1%; Pred. No. 1.9e-64;
 Matches 153; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
 QY 2 PPAPRLICDSRVLYRLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 61
 DB 26 PGAPRLICDSRVLYRLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 85
 QY 62 QAVEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGRLSLTTLRALGAQKEA 121
 DB 86 QAVEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGRLSLTTLRALGAQ-EA 144
 QY 122 ISPPDAASAPLRTITADTFKRLFRVYSNFKLGLKLYTGEACRTGDR 169
 DB 145 ISLPDAASAPLRTITADTFKRLFRVYSNFKLGLKLYTGEACRTGDR 192

RESULT 4

EPO_MACMU STANDARD; PRT; 192 AA.

AC Q28513;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=EPO;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 RA Czelusniak J., Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 RT sequence homology among mammals.";
 RL Blood 82:1507-1516(1993)
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 CC regulation of erythrocyte differentiation and the maintenance of a
 CC physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 CC and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.

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 CC EMBL; L10609; AAA36842.1; -;
 DR PIR; I84613; I84613.
 DR HSSP; P01588; ICN4.
 DR InterPro; IPR009079; 4 helix_cytokine.
 DR InterPro; IPR001323; EPO.TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO.TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO.TPO; 1.
 DR PROSITE; PS00817; EPO.TPO; 1.
 DR SEQUENCE 192 AA; 275560A364628CD1 CRC64;

Query Match 88.6%; Score 769.5; DB 1; Length 192;
 Best Local Similarity 89.9%; Pred. No. 5.5e-64;
 Matches 151; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 2 PPAPPLICDSRVLYLLRAKEAENITTCAGHCSLNENITVPTDKVNFYAKRMEVQ 61
 DB 26 PGAPPLVCDSRVLYLLRAKEAENITTCAGHCSLNENITVPTDKVNFYAKRMEVQ 85
 QY 62 QAVEVWQGLALLSAVLRGQAVLNVSSQPWEPLQLHVDKAVSGRLSITLLRALGAKEA 121
 DB 86 QAVEVWQGLALLSAVLRGQAVLNVSSQPWEPLQLHVDKAVSGRLSITLLRALGAQ-EA 144

Query Match 88.6%; Score 769.5; DB 1; Length 192;
 Best Local Similarity 89.9%; Pred. No. 5.5e-64;
 Matches 151; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 122 ISPPDAAGAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 169
 DB 145 ISLPDAAGAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 192

RESULT 5

Q867B1 PRELIMINARY; PRT; 192 AA.

AC Q867B1;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Erythropoietin.
 GN Name=EPO;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX PubMed=14719696;
 RA Sato F., Yamashita S., Kugo T., Hasegawa T., Mitsui I.,
 RA Kijima-Suda I.;
 RT "Nucleotide sequence of equine erythropoietin and characterization of
 RT region-specific antibodies.";
 RL Am. J. Vet. Res. 65:15-19(2004).
 DR EMBL; AB100030; BAC55239.1; -;
 DR HSSP; P01588; 1BUY.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR009079; 4 helix_cytokine.
 DR InterPro; IPR001323; EPO.TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO.TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO.TPO; 1.
 DR PROSITE; PS00817; EPO.TPO; 1.
 DR SEQUENCE 192 AA; 20984 MW; E02D098490B09C4F CRC64;

Query Match 83.8%; Score 728.5; DB 2; Length 192;
 Best Local Similarity 81.7%; Pred. No. 3.9e-60;
 Matches 143; Conservative 10; Mismatches 15; Indels 7; Gaps 1;

QY 2 PP-----APPLICDSRVLYLLRAKEAENITTCAGHCSLNENITVPTDKVNFYAW 54
 DB 18 PPLGLPALGAPPLICDSRVLYLLRAKEAENITTCAGHCSLNENITVPTDKVNFYAW 77

QY 55 KRMEVQQAQVEVWQGLALLSAVLRGQAVLNVSSQPWEPLQLHVDKAVSGRLSITLLRA 114
 DB 78 KRMEVQQAQVEVWQGLALLSAVLRGQAVLNVSSQPWEPLQLHVDKAVSGRLSITLLRA 137
 QY 115 LGAQKEAISPPDAASAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 169
 DB 138 LGAQKEAISPPDAASAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 192

RESULT 6

EPO_FELCA STANDARD; PRT; 192 AA.

AC P33708;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=EPO;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;
 RA Goodman R.E., Bell R.G.;
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 5-192 FROM N.A.
 RX MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 RA Czelusniak J., Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 RT sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 CC regulation of erythrocyte differentiation and the maintenance of a
 CC physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 CC and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
 CC
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 CC
 CC EMBL; U00685; AAA18282.1; -;
 DR EMBL; L10606; AAA30807.1; -;
 DR PIR; I46083; I46083.
 DR HSSP; P01588; I46083.
 DR
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 DR Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 KW SIGNAL 1 26 By similarity.
 FT CHAIN 27 192 Erythropoietin.
 FT DISULFID 33 187 By similarity.
 FT DISULFID 55 59 By similarity.
 FT CARBOHYD 50 50 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 64 64 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 44 44 G -> E (in Ref. 2).
 SQ SEQUENCE 192 AA; 20914 MW; 61C5EA0F5E937293 CRC64;
 Query Match 81.8%; Score 711; DB 1; Length 192;
 Best Local Similarity 83.7%; Pred. No. 1.7e-58;
 Matches 139; Conservative 9; Mismatches 18; Indels 0; Gaps 0;
 QY 4 APRRLICDSRVLYRLLEAKAEENITTCGAHCNSLNENITVPTKYNFYAKRMEVGQQA 63
 DB 27 APRRLICDSRVLYRLLEAKAEENITTCGAHCNSLNENITVPTKYNFYAKRMEVGQQA 86
 QY 64 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGRLSTLTLLRALGAQKEATS 123
 DB 87 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGRLSTLTLLRALGAQKEATS 146
 QY 124 PPDAASAPLRTITADTFKFLRVYSNLFRLGKLYTGACRTGDR 169
 DB 147 LEATSAAPLRTITADTFKFLRVYSNLFRLGKLYTGACRTGDR 192
 RESULT 7
 EPO RAT
 AC P29576; P70504; PRT; 192 AA.
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Erythropoietin precursor.
 GN Name=Epo;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Kidney;
 RX MEDLINE=93042015; PubMed=1420369;
 RA Nagao M., Suga H., Okano M., Masuda S., Narita H., Ikura K.,
 RA Sasaki R.;
 RT "Nucleotide sequence of rat erythropoietin.";
 RL Biochim. Biophys. Acta 1171:99-102(1992).
 RN [2]
 RP SEQUENCE OF 4-192 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
 RX MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Boissel J.P.R., Tracy T.E., Mulcahy L.S., Czelusniak J.,
 RA Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 RT sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 CC regulation of erythrocyte differentiation and the maintenance of a
 CC physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 CC and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
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 CC EMBL; D10763; BAA01593.1; -;
 DR EMBL; L10608; AAA41126.1; -;
 DR PIR; S28148; S28148.
 DR HSSP; P01588; ICA4.
 DR RGD; 2559; EPO.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 DR Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 KW SIGNAL 1 26 By similarity.
 FT CHAIN 27 192 Erythropoietin.
 FT DISULFID 33 187 By similarity.
 FT CARBOHYD 50 50 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 64 64 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 109 109 N-linked (GlcNAc...) (By similarity).
 SQ SEQUENCE 192 AA; 21286 MW; 3EA632737E7D2443 CRC64;
 Query Match 81.2%; Score 706; DB 1; Length 192;
 Best Local Similarity 82.5%; Pred. No. 5e-58;
 Matches 137; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
 QY 4 APRRLICDSRVLYRLLEAKAEENITTCGAHCNSLNENITVPTKYNFYAKRMEVGQQA 63
 DB 27 APRRLICDSRVLYRLLEAKAEENITTCGAHCNSLNENITVPTKYNFYAKRMEVGQQA 86
 QY 64 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGRLSTLTLLRALGAQKEATS 123
 DB 87 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGRLSTLTLLRALGAQKEATS 146
 QY 124 PPDAASAPLRTITADTFKFLRVYSNLFRLGKLYTGACRTGDR 169

Query	Match	Conservative	Mismatches	Indels	Gaps
4 APPRLICDSRLVRLERYLLLEAKAEENITTGCAAEHCISLNENITVPDITKKNFYAWKRMVEYGOOA	63	135	13	18	0

RA Czelusniak J., Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
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CC -----
CC EMBL; Z24681; CAAB0848.1; -;
CC EMBL; LI0610; AAA31518.1; -;
CC PIR; I46401; I46401.
CC HSP; P01588; 1CN4.
CC InterPro; IPR009079; 4 helix_cytokine.
CC InterPro; IPR001323; EPO_TPO.
CC InterPro; IPR003013; Erythroptn.
CC Pfam; PF00758; EPO_TPO; 1.
CC PIRSF; PIRSF001951; EPO; 1.
CC PRINTS; PR00272; ERYTHROPTN.
CC PROSITE; PS00817; EPO_TPO; 1.
CC Erythrocyte maturation; Glycoprotein; Hormone; Signal.
KW SIGNAL 1 27
FT CHAIN 28 194
FT DISULFID 34 189
FT DISULFID 56 60
FT CARBOHYD 51 51
FT CARBOHYD 65 65
FT CARBOHYD 110 110
FT CONFLICT 16 16
FT CONFLICT 108 108
FT SEQUENCE 194 AA; 21335 MW; C025AAB0528131A9 CRC64;
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 27
FT CHAIN 28 194
FT DISULFID 34 189
FT DISULFID 56 60
FT CARBOHYD 51 51
FT CARBOHYD 65 65
FT CARBOHYD 110 110
FT CONFLICT 16 16
FT CONFLICT 108 108
FT SEQUENCE 194 AA; 21335 MW; C025AAB0528131A9 CRC64;
Query Match 79.5%; Score 690.5; DB 1; Length 194;
Best Local Similarity 82.0%; Pred. No. 1.4e-56;
Matches 137; Conservative 9; Mismatches 20; Indels 1; Gaps 1;
QY 4 APPRLICDSRVLELYLEAKEAENITTCGAHCNLSNENITVPDTKYNFYAKRMEVQQA 63
DB 28 APPRLICDSRVLELYLEAKEAENITTCGAHCNLSNENITVPDTKYNFYAKRMEVQQA 87
QY 64 VEVWQGLALLSEAVLRQALLVNSQPWEPQLQHVDAKAVSLRLTLLRALGAQKEAIS 123
DB 88 LEVWQGLALLSEAVLRQALLVNSQPWEPQLQHVDAKAVSLRLTLLRALGAQKEAIP 147
QY 124 PDAAA-SAAPLRTITADTFKFLFRVYNSFLRGKLYTGACRTGDR 169
DB 148 LPDAPSAAPLRTITADTFKFLFRVYNSFLRGKLYTGACRTGDR 194
RESULT 13
Q9GKA2 PRELIMINARY; PRT; 195 AA.
AC Q9GKA2
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Erythropoietin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CX NCBI_TaxID=9986;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=21290682; PubMed=11396976;
RT Vilalta A., Wu D., Margalith M., Hobart P.;
RT "Rabbit EPO gene and cDNA: expression of rabbit EPO after
RT intramuscular injection of pDNA.";
RL Biochem. Biophys. Res. Commun. 284:823-827(2001).
DR EMBL; AF290944; AAG36962.1; -;
DR HSP; P01588; 1CN4.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR009079; 4 helix_cytokine.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PIRSF; PIRSF001951; EPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
SQ SEQUENCE 195 AA; 21025 MW; 1F1DC7F403A303EC CRC64;
Query Match 78.9%; Score 685.5; DB 2; Length 195;
Best Local Similarity 81.4%; Pred. No. 4.3e-56;
Matches 136; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
QY 4 APPRLICDSRVLELYLEAKEAENITTCGAHCNLSNENITVPDTKYNFYAKRMEVQQA 63
DB 29 APPRLICDSRVLELYLEAKEAENITTCGAHCNLSNENITVPDTKYNFYAKRMEVQQA 88
QY 64 VEVWQGLALLSEAVLRQALLVNSQPWEPQLQHVDAKAVSLRLTLLRALGAQKEAIS 123
DB 89 VEVWQGLALLSEAVLRQALLVNSQPWEPQLQHVDAKAVSLRLTLLRALGAQKEAIS 148
QY 124 PDAAA-SAAPLRTITADTFKFLFRVYNSFLRGKLYTGACRTGDR 169
DB 149 PPEAASSAAPLRTITADTFKFLFRVYNSFLRGKLYTGACRTGDR 195
RESULT 14
Q9GKA3 PRELIMINARY; PRT; 195 AA.
AC Q9GKA3
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Erythropoietin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21290682; PubMed=11396976;
RT Vilalta A., Wu D., Margalith M., Hobart P.;
RT "Rabbit EPO gene and cDNA: expression of rabbit EPO after
RT intramuscular injection of pDNA.";
RL Biochem. Biophys. Res. Commun. 284:823-827(2001).
DR EMBL; AF290943; AAG36961.1; -;
DR PIR; JC7699; JC7699.
DR HSP; P01588; 1CN4.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR009079; 4 helix_cytokine.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PIRSF; PIRSF001951; EPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
SQ SEQUENCE 195 AA; 21053 MW; 0999DA7D852713F3 CRC64;
Query Match 78.9%; Score 685.5; DB 2; Length 195;
Best Local Similarity 81.4%; Pred. No. 4.3e-56;
RN [1]

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Matches 136; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
QY 4 APPRLICDSRVLERYLLLEAKAENITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGQA 63
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 29 APARLICDSRVLERYLLLEAKAENITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGQA 88
QY 64 VEVWQGLALLSEAVLRGQALLVNSSQWPPELQLHVDKAVSGLSRLTLLRALGAKQEAIS 123
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 89 VEVWQGLALLSEAVLRGQALLVNSSQWPPELQLHVDKAVSGLSRLTLLRALGAKQEAIS 148
QY 124 PPDA--SNAAPLRTITADTFKLFVYSNLFRLGKLYTGACRTGDR 169
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 149 PPEAASAAPLRTVAADTLCKLFRIYSNLFRLGKLYTGACRTGDR 195

RESULT 15
EPO_PIG STANDARD; PRT; 190 AA.
AC P49157;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Erythropoietin precursor (Fragment).
GN Name=EPO;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
RA Czelusniak J., Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -|- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -|- SIMILARITY: Belongs to the EPO / TPO family.
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CC -----
DR EMBL; L10607; AAA31029.1; -
DR EIR; I46578; I46578.
DR HSSP; P01588; 1CN4.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythropo.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; ERYTHROPTN.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT NON_TER 1
FT SIGNAL 22
FT CHAIN 23
FT CHAIN 190
FT DISULFID 29
FT DISULFID 51
FT CARBOHYD 46
FT CARBOHYD 60
FT CARBOHYD 105
FT CARBOHYD 168
FT CARBOHYD 168
FT SEQUENCE 190 AA; 20888 MW; A75BD6CCE5077E2A CRC64;
SQ
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Query Match 78.6%; Score 683; DB 1; Length 190;
Best Local Similarity 82.1%; Pred. No. 7.1e-56;
Matches 138; Conservative 7; Mismatches 21; Indels 2; Gaps 1;
QY 4 APPRLICDSRVLERYLLLEAKAENITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGQA 63
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 APPRLICDSRVLERYLLLEAKAENITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGQA 82
QY 64 VEVWQGLALLSEAVLRGQALLVNSSQWPPELQLHVDKAVSGLSRLTLLRALGAKQEAIS 123
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 VEVWQGLALLSEAVLRGQALLVNSSQWPPELQLHVDKAVSGLSRLTLLRALGAKQEAIS 142
QY 124 PPDA--ASAAPLRTITADTFKLFVYSNLFRLGKLYTGACRTGDR 169
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 143 LPDASPSSATPLRTFAVDTLCKLFRIYSNLFRLGKLYTGACRTGDR 190
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Search completed: November 19, 2004, 21:10:59
Job time : 102.008 secs

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OM protein - protein search, using sw model

Run on: November 19, 2004, 20:57:38 ; Search time 61.2534 Seconds
(without alignments)
1019.028 Million cell updates/sec

Title: US-10-014-363-5

Perfect score: 898

Sequence: 1 APPGAHYAPRLICDSRVL.....NFLRGKLYTGACRTGDR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003s:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB Length	ID	Description
1	898	100.0	174	5	ABB77900	Abb77900 Amino aci
2	898	100.0	201	5	ABB77903	Abb77903 Amino aci
3	861	95.9	174	5	ABB77898	Abb77898 Amino aci
4	861	95.9	201	5	ABB77901	Abb77901 Amino aci
5	857	95.4	205	8	ADJ71846	Adj71846 Non-glyco
6	856.5	95.4	169	5	ABB77899	Abb77899 Amino aci
7	856.5	95.4	196	5	ABB77902	Abb77902 Amino aci
8	854	95.1	376	2	AAW99360	AAw99360 Human ery
9	852	94.9	167	2	AAW71251	AAw71251 Human ery
10	852	94.9	769	7	ADF15091	Adf15091 Human alb
11	851	94.8	166	1	AAW70398	AAw70398 Sequence
12	851	94.8	166	2	AAW23593	AAw23593 Recombina
13	851	94.8	166	2	AAW58404	AAw58404 Human ery
14	851	94.8	166	2	AAW77780	AAw77780 Human EPO
15	851	94.8	166	3	ABB07030	Abb07030 Modified
16	851	94.8	166	4	ABB83622	Abb83622 Protein #
17	851	94.8	166	4	AAE02841	AAe02841 Human ery
18	851	94.8	166	4	AAE66698	AAe66698 Human ery
19	851	94.8	166	5	ABG92101	ABg92101 Human ery
20	851	94.8	166	5	AAW53062	AAw53062 Human ery
21	851	94.8	166	5	ABB77897	Abb77897 Human ery
22	851	94.8	166	5	ADG65661	Adg65661 Human aci
23	851	94.8	166	6	ABR39996	ABr39996 Human ery
24	851	94.8	166	6	ABR57500	ABr57500 Human ery
25	851	94.8	166	7	ADF70839	Adf70839 Human ery

26	851	94.8	166	8	ADL92150	Adl92150 Erythropo
27	851	94.8	166	8	ADK70564	Adk70564 Human ery
28	851	94.8	166	8	ADL88867	Adl88867 Human cyt
29	851	94.8	166	8	ADL06781	Adl06781 Human 166
30	851	94.8	166	8	ADO59416	Ado59416 Human 166
31	851	94.8	167	1	AAW50299	AAw50299 Human rec
32	851	94.8	167	1	AAW50298	AAw50298 Human lam
33	851	94.8	188	1	AAW60599	AAw60599 Clone lam
34	851	94.8	188	1	AAW61195	AAw61195 Erythropo
35	851	94.8	193	1	AAW50300	AAw50300 Human ery
36	851	94.8	193	1	AAW60597	AAw60597 Clone lam
37	851	94.8	193	1	AAW70256	AAw70256 Sequence
38	851	94.8	193	2	AAW65499	AAw65499 Human pre
39	851	94.8	193	2	AAW71137	AAw71137 Human ery
40	851	94.8	193	2	AAW74141	AAw74141 Human ery
41	851	94.8	193	2	AAW81982	AAw81982 Human ery
42	851	94.8	193	2	AAW98397	AAw98397 Human ery
43	851	94.8	193	3	AAW43398	AAw43398 Human ery
44	851	94.8	193	3	AAW94530	AAw94530 Human ery
45	851	94.8	193	3	AAW93638	AAw93638 Amino aci

ALIGNMENTS

RESULT 1
ABB77900

ID ABB77900 standard; protein; 174 AA.

XX ABB77900;

DT 07-OCT-2002 (first entry)

XX Amino acid sequence of a modified human erythropoietin (EPO).

KW Human; erythropoietin; EPO; glycoprotein; reticulocyte production;

KW red blood cell production; anaemia; chronic renal failure;

KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;

KW committed erythroid progenitor.

XX Synthetic.

OS Homo sapiens.

FX Key Location/Qualifiers

FT Cleavage-site 1..8

FT Protein /note= "proteolytic cleavage site"

FT Protein 9..174

FT Protein /note= "EPO protein"

XX WO200249673-A2.

PD 27-JUN-2002.

XX 08-DEC-2001; 2001WO-EP014434.

XX 20-DEC-2000; 2000EP-00127891.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;

XX Wozny M;

XX WPI; 2002-566640/60.

XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol, useful for treating diseases correlated with anemia in chronic renal failure patients and acquired immunodeficiency syndrome.

XX Disclosure; Page 39-40; 40pp; English.

XX The present sequence represents a modified human erythropoietin (EPO) protein. The EPO was extended at the N-terminal by a proteolytic cleavage site. It was used to produce conjugates of the invention. The

CC specification describes a conjugate comprising an EPO glycoprotein having
 CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 CC or a rearrangement of a glycosylation site). The glycoprotein is
 CC covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 CC has in vivo biological activity of causing bone marrow cells to increase
 CC production of reticulocytes and red blood cells. The conjugate increases
 CC circulating half-life and plasma residence time, decreased clearance,
 CC increased clinical activity in vivo, improved potency and stability, when
 CC compared to unmodified EPO. The EPO conjugate is useful for preparing
 CC medicaments for the treatment and prophylaxis of diseases correlated with
 CC anaemia in chronic renal failure patients (CRF), acquired
 CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow

XX Sequence 174 AA;

Query Match 100.0%; Score 898; DB 5; Length 174;
 Best Local Similarity 100.0%; Pred. No. 1.5e-89;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPGAHYAPPLICDSRVLYLLEAKEAENITTCABHCSLNENITVDTKVFYAWK 60
 DB 1 APPGAHYAPPLICDSRVLYLLEAKEAENITTCABHCSLNENITVDTKVFYAWK 60

QY 61 RMEVGQAVVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTLRAL 120
 DB 61 RMEVGQAVVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTLRAL 120

QY 121 GAOKEAISPPDAASAAPLRTITADTRKLFVYSNFRGLKLYTGEACRTGDR 174
 DB 121 GAOKEAISPPDAASAAPLRTITADTRKLFVYSNFRGLKLYTGEACRTGDR 174

QY 07-OCT-2002 (first entry)

DE Amino acid sequence of a modified human erythropoietin (EPO).

XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.

XX Synthetic.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..27
 FT /note= "secretion signal peptide"
 FT Cleavage-site 28..35
 FT /note= "proteolytic cleavage site"
 FT Protein 36..201
 FT /note= "EPO protein"

XX WO200249673-A2.

XX 27-JUN-2002.

XX 08-DEC-2001; 2001WO-EP014434.

XX 20-DEC-2000; 2000EP-00127891.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;

PI Wozny M;

XX WPI; 2002-566640/60.
 DR N-P5DB; ABUS9291.

XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 PT useful for treating diseases correlated with anemia in chronic renal
 PT failure patients and acquired immunodeficiency syndrome.

XX Disclosure; Fig 5; 40pp; English.

XX The present sequence represents a modified human erythropoietin (EPO)
 CC protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 CC site. It was used to produce conjugates of the invention. The
 CC specification describes a conjugate comprising an EPO glycoprotein having
 CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 CC or a rearrangement of a glycosylation site). The glycoprotein is
 CC covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 CC has in vivo biological activity of causing bone marrow cells to increase
 CC production of reticulocytes and red blood cells. The conjugate increases
 CC circulating half-life and plasma residence time, decreased clearance,
 CC increased clinical activity in vivo, improved potency and stability, when
 CC compared to unmodified EPO. The EPO conjugate is useful for preparing
 CC medicaments for the treatment and prophylaxis of diseases correlated with
 CC anaemia in chronic renal failure patients (CRF), acquired
 CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow

XX Sequence 201 AA;

Query Match 100.0%; Score 898; DB 5; Length 201;
 Best Local Similarity 100.0%; Pred. No. 1.9e-89;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPGAHYAPPLICDSRVLYLLEAKEAENITTCABHCSLNENITVDTKVFYAWK 60
 DB 28 APPGAHYAPPLICDSRVLYLLEAKEAENITTCABHCSLNENITVDTKVFYAWK 87

QY 61 RMEVGQAVVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTLRAL 120
 DB 88 RMEVGQAVVEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSLTLRAL 147

QY 121 GAOKEAISPPDAASAAPLRTITADTRKLFVYSNFRGLKLYTGEACRTGDR 174
 DB 148 GAOKEAISPPDAASAAPLRTITADTRKLFVYSNFRGLKLYTGEACRTGDR 201

RESULT 3

ABB77898 standard; protein; 174 AA.

XX ABB77898;

XX 07-OCT-2002 (first entry)

DE Amino acid sequence of a modified human erythropoietin (EPO).

XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.

XX Synthetic.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Cleavage-site 1..8
 FT /note= "proteolytic cleavage site"
 FT Protein 9..174
 FT /note= "EPO protein"

KW WO200249673-A2.
 PN 27-JUN-2002.
 XX 08-DEC-2001; 2001WO-EP014434.
 XX 20-DEC-2000; 2000EP-00127891.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 XX Wozny M;
 XX WPI; 2002-566640/60.
 XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 XX useful for treating diseases correlated with anemia in chronic renal
 XX failure patients and acquired immunodeficiency syndrome.
 XX Disclosure; Page 38-39; 40pp; English.
 XX The present sequence represents a modified human erythropoietin (EPO)
 XX protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 XX site. It was used to produce conjugates of the invention. The
 XX specification describes a conjugate comprising an EPO glycoprotein having
 XX an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 XX analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 XX or a rearrangement of a glycosylation site). The glycoprotein is
 XX covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 XX has in vivo biological activity of causing bone marrow cells to increase
 XX production of reticulocytes and red blood cells. The conjugate increased
 XX circulating half-life and plasma residence time, decreased clearance,
 XX increased clinical activity in vivo, improved potency and stability, when
 XX compared to unmodified EPO. The EPO conjugate is useful for preparing
 XX medicaments for the treatment and prophylaxis of diseases correlated with
 XX anaemia in chronic renal failure patients (CRF), acquired
 XX immunodeficiency syndrome (AIDS) and for treating cancer patients
 XX undergoing chemotherapy. It is also useful for treating patients by
 XX stimulating the division and differentiation of committed erythroid
 XX progenitors in the bone marrow
 XX Sequence 174 AA;

Query Match 95.9%; Score 861; DB 5; Length 174;
 Best Local Similarity 97.1%; Pred. No. 1.7e-85;
 Matches 169; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 APPGAHYAPPLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWK 60
 DB 1 APPRIEGRAPPLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWK 60
 QY 61 RMEVQQQAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRAL 120
 DB 61 RMEVQQQAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRAL 120
 QY 121 GAOKEAISPPDAASAAPLRTITADTFKLFVYSNLFRLGKLYTGEACRTGDR 174
 DB 121 GAOKEAISPPDAASAAPLRTITADTFKLFVYSNLFRLGKLYTGEACRTGDR 174

RESULT 4
 ID ABB77901
 XX ABB77901 standard; protein; 201 AA.
 AC ABB77901;
 XX 07-OCT-2002 (first entry)
 DT Amino acid sequence of a modified human erythropoietin (EPO).
 DE Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 XX red blood cell production; anaemia; chronic renal failure;
 KW

KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.
 OS Synthetic.
 OS Homo sapiens.
 PH Key Location/Qualifiers
 FT 1..27
 FT /note= "secretion signal peptide"
 FT 28..35
 FT /note= "proteolytic cleavage site"
 FT 36..201
 FT /note= "EPO protein"
 XX WO200249673-A2.
 PN 27-JUN-2002.
 XX 08-DEC-2001; 2001WO-EP014434.
 XX 20-DEC-2000; 2000EP-00127891.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 XX Wozny M;
 XX WPI; 2002-566640/60.
 XX N-PSDB; ABL59289.
 XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 XX useful for treating diseases correlated with anemia in chronic renal
 XX failure patients and acquired immunodeficiency syndrome.
 XX Disclosure; Fig 3; 40pp; English.
 XX The present sequence represents a modified human erythropoietin (EPO)
 XX protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 XX site. It was used to produce conjugates of the invention. The
 XX specification describes a conjugate comprising an EPO glycoprotein having
 XX an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 XX analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 XX or a rearrangement of a glycosylation site). The glycoprotein is
 XX covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 XX has in vivo biological activity of causing bone marrow cells to increase
 XX production of reticulocytes and red blood cells. The conjugate increased
 XX circulating half-life and plasma residence time, decreased clearance,
 XX increased clinical activity in vivo, improved potency and stability, when
 XX compared to unmodified EPO. The EPO conjugate is useful for preparing
 XX medicaments for the treatment and prophylaxis of diseases correlated with
 XX anaemia in chronic renal failure patients (CRF), acquired
 XX immunodeficiency syndrome (AIDS) and for treating cancer patients
 XX undergoing chemotherapy. It is also useful for treating patients by
 XX stimulating the division and differentiation of committed erythroid
 XX progenitors in the bone marrow
 XX Sequence 201 AA;

Query Match 95.9%; Score 861; DB 5; Length 201;
 Best Local Similarity 97.1%; Pred. No. 2.1e-85;
 Matches 169; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 APPGAHYAPPLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWK 60
 DB 28 APPRIEGRAPPLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWK 87
 QY 61 RMEVQQQAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRAL 120
 DB 88 RMEVQQQAVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLLRAL 147
 QY 121 GAOKEAISPPDAASAAPLRTITADTFKLFVYSNLFRLGKLYTGEACRTGDR 174
 DB 148 GAOKEAISPPDAASAAPLRTITADTFKLFVYSNLFRLGKLYTGEACRTGDR 201

RESULT 6
ABB77899
ID ABB77899 standard; protein; 169 AA.
XX
AC ABB77899;
XX
DT 07-OCT-2002 (first entry)
XX
DE Amino acid sequence of a modified human erythropoietin (EPO).
XX
KW Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
KW red blood cell production; anaemia; chronic renal failure;
KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
KW committed erythroid progenitor.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Cleavage-site 1..3
FT /note= "proteolytic cleavage site"
FT Protein 4..174
FT /note= "EPO protein"
XX
XX WO200249673-A2.
XX
XX
XX 27-JUN-2002.
XX
XX 08-DEC-2001; 2001WO-EP014434.
XX
XX 20-DEC-2000; 2000EP-00127891.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
XX Wozny M;
XX
XX MPI; 2002-566640/60.
XX
XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
XX useful for treating diseases correlated with anemia in chronic renal
XX failure patients and acquired immunodeficiency syndrome.
XX
XX Disclosure; Page 39; 40pp; English.
XX
XX The present sequence represents a modified human erythropoietin (EPO)
XX protein. The EPO was extended at the N-terminal by a proteolytic cleavage
XX site. It was used to produce conjugates of the invention. The
XX specification describes a conjugate comprising an EPO glycoprotein having
XX an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
XX analogues (where hEPO is modified by addition of 1-6 glycosylation sites
XX or a rearrangement of a glycosylation site). The glycoprotein is
XX covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
XX has in vivo biological activity of causing bone marrow cells to increase
XX production of reticulocytes and red blood cells. The conjugate increased
XX circulating half-life and plasma residence time, decreased clearance, when
XX increased clinical activity in vivo, improved potency and stability, when
XX compared to unmodified EPO. The EPO conjugate is useful for preparing
XX medicaments for the treatment and prophylaxis of diseases correlated with
XX anaemia in chronic renal failure patients (CRF), acquired
XX immunodeficiency syndrome (AIDS) and for treating cancer patients
XX undergoing chemotherapy. It is also useful for treating patients by
XX stimulating the division and differentiation of committed erythroid
XX progenitors in the bone marrow
XX
XX Sequence 169 AA;

QY 1 APPGAHYAPRLICDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKNVFAWK 60
 DB 1 APP-----APRLICDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKNVFAWK 55
 QY 61 RMEVGQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLLTLRAL 120
 DB 56 RMEVGQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLLTLRAL 115
 QY 121 GAQKEAISPPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 174
 DB 116 GAQKEAISPPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 169

RESULT 7
 ABB77902
 ID ABB77902 standard; protein; 196 AA.
 XX AC ABB77902;
 XX DT 07-OCT-2002 (first entry)
 DE Amino acid sequence of a modified human erythropoietin (EPO).
 XX Human: erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.
 XX Synthetic.
 OS Homo sapiens.
 XX FH Key
 FT Peptide Location/Qualifiers
 FT 1..27 /note= "secretion signal peptide"
 FT Cleavage-site 28..30 /note= "proteolytic cleavage site"
 FT Protein 31..196 /note= "EPO protein"
 FT WO200249673-A2.
 PN 27-JUN-2002.
 PD 08-DEC-2001; 2001WO-EP014434.
 XX 20-DEC-2000; 2000EP-00127891.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischler W;
 PI Wozny M;
 XX WPI; 2002-566640/60.
 DR N-PSDB; ABL59290.
 XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 PT useful for treating diseases correlated with anemia in chronic renal
 PT failure patients and acquired immunodeficiency syndrome.
 XX Disclosure; Fig 4; 40pp; English.

CC The present sequence represents a modified human erythropoietin (EPO)
 CC protein. The EPO was extended at the N-terminal by a proteolytic cleavage
 CC site. It was used to produce conjugates of the invention. The
 CC specification describes a conjugate comprising an EPO glycoprotein having
 CC an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
 CC analogues (where hEPO is modified by addition of 1-6 glycosylation sites
 CC or a rearrangement of a glycosylation site). The glycoprotein is
 CC covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein
 CC has in vivo biological activity of causing bone marrow cells to increase
 CC production of reticulocytes and red blood cells. The conjugate increased
 CC circulating half-life and plasma residence time, decreased clearance,
 CC increased clinical activity in vivo, improved potency and stability, when

CC compared to unmodified EPO. The EPO conjugate is useful for preparing
 CC medicaments for the treatment and prophylaxis of diseases correlated with
 CC anaemia in chronic renal failure patients (CRF), acquired
 CC immunodeficiency syndrome (AIDS) and for treating cancer patients
 CC undergoing chemotherapy. It is also useful for treating patients by
 CC stimulating the division and differentiation of committed erythroid
 CC progenitors in the bone marrow

SQ Sequence 196 AA;

Query Match 95.4%; Score 856.5; DB 5; Length 196;
 Best Local Similarity 97.1%; Pred. No. 6.2e-85;
 Matches 169; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 APPGAHYAPRLICDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKNVFAWK 60
 DB 28 APP-----APRLICDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKNVFAWK 82
 QY 61 RMEVGQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLLTLRAL 120
 DB 83 RMEVGQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLLTLRAL 142
 QY 121 GAQKEAISPPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 174
 DB 143 GAQKEAISPPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 196

RESULT 8

AAW99360
 ID AAW99360 standard; protein; 376 AA.

XX AC AAW99360;

XX DT 21-MAY-1999 (first entry)

XX Human erythropoietin homodimer fusion protein.

KW Human; erythropoietin; dimer; trimer; polymer; fusion protein; cancer;
 KW biological activity; anaemia; proliferation; differentiation; progenitor;
 KW leucocyte; granulocyte; blood; myelosuppressed patient.

OS Homo sapiens.

OS Synthetic.

PN WO9902710-A1.

XX 21-JAN-1999.

PF 09-JUL-1998; 98WO-US013944.

PR 10-JUL-1997; 97US-00890929.

PR 03-FEB-1998; 98US-00018138.

PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

PI Sytkowski AJ;

XX WPI; 1999-120911/10.

DR N-PSDB; AAX25701.

PT New fusion protein with increased activity comprising at least two
 PT protein molecules - used to, e.g. treat erythropoietin related deficiency
 PT states for treatment of anaemia.

XX Example 1; Fig 16A-C; 119pp; English.

PS This sequence represents a human erythropoietin (EPO) homodimeric fusion
 CC protein. The invention relates to the production of dimeric, trimeric or
 CC polymeric fusion proteins with increased biological activity. The fusion
 CC proteins are used to treat or prevent protein-related deficiency states,
 CC specifically, where the protein is erythropoietin (EPO; AAX25689),
 CC anaemia, but also for increasing proliferation, differentiation and
 CC activity of haematopoietic progenitors (e.g. increasing numbers of

CC leucocytes and granulocytes in the blood of myelosuppressed patients) or
CC for treating cancer and other cell growth disorders
XX
SQ Sequence 376 AA;

Query Match 95.1%; Score 854; DB 2; Length 376;
Best Local Similarity 97.7%; Pred. No. 2.9e-84;
Matches 167; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 GAAYVAPPRLLICDSRVLYRLLLEAEAEENITTCGAHCHSLNENITVPDTKVNIFYAKRME 63
Db 206 GGGSTAPPRLICDSRVLYRLLLEAEAEENITTCGAHCHSLNENITVPDTKVNIFYAKRME 265
QY 64 VQQAQVEVWQGLALLSEAVLRGALLVNSQWPEPLQLHVDKAVSLRSLTLLRALGQ 123
Db 266 VQQAQVEVWQGLALLSEAVLRGALLVNSQWPEPLQLHVDKAVSLRSLTLLRALGQ 325
QY 124 KEAISPPDAASAAPLRTITADTFRKLFRVYSNPLRGKLYTGEACRTGDR 174
Db 326 KEAISPPDAASAAPLRTITADTFRKLFRVYSNPLRGKLYTGEACRTGDR 376

RESULT 9
AAR71251
ID AAR71251 standard; protein; 167 AA.
XX
AC AAR71251;
XX
DT 25-MAR-2003 (revised)
DT 01-NOV-1995 (first entry)
XX
DE Human erythropoietin analogue Ser103.
XX
KW Human erythropoietin; glycosylation; sialic acid; solubility; half-life;
KW biological activity; proteolysis resistance; anaemia;
KW chronic renal failure; analogue Ser103; O-linked carbohydrate chain.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Binding-site 103
FT /note= "O-linked glycosylation site"
XX
PN W09505465-A1.
XX
PD 23-FEB-1995.
XX
PF 16-AUG-1994; 94WO-US009257.
XX
PR 17-AUG-1993; 93US-00108016.
XX
PA (AMGE-) AMGEN INC.
XX
PI Elliott SG, Byrne TE;
XX
DR WPI; 1995-098764/13.
XX
XX Erythropoietin (EPO) analogues having additional glycosylation site(s) -
PT to increase sialic acid content, thereby increasing solubility, serum
PT half-life, biological activity and resistance to proteolysis.
XX
PS Claim 3; Fig 5; 108pp; English.
XX
CC AAR71223-R71283 are human erythropoietin (EPO) analogues, they have at
CC least one additional glycosylation site (compared to the wild type EPO),
CC for the addition of a O-linked carbohydrate chain. This is used to
CC increase the sialic acid content which in turn increases the solubility,
CC half-life, biological activity and proteolysis resistance of the protein.
CC The analogues are useful in claimed compens. for the treatment of chronic
CC renal failure associated anaemia. (Updated on 25-MAR-2003 to correct PN
XX field.)
SQ Sequence 167 AA;

Query Match 94.9%; Score 852; DB 2; Length 167;
Best Local Similarity 99.4%; Pred. No. 1.5e-84;
Matches 166; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 YAPPRLLICDSRVLYRLLLEAEAEENITTCGAHCHSLNENITVPDTKVNIFYAKRMEVGOO 67
Db 1 YAPPRLLICDSRVLYRLLLEAEAEENITTCGAHCHSLNENITVPDTKVNIFYAKRMEVGOO 60
QY 68 AVEVWQGLALLSEAVLRGALLVNSQWPEPLQLHVDKAVSLRSLTLLRALGQKEAI 127
Db 61 AVEVWQGLALLSEAVLRGALLVNSQWPEPLQLHVDKAVSLRSLTLLRALGQKEAI 120
QY 128 SPDDAASAAPLRTITADTFRKLFRVYSNPLRGKLYTGEACRTGDR 174
Db 121 SPDDAASAAPLRTITADTFRKLFRVYSNPLRGKLYTGEACRTGDR 167
RESULT 10
ADF15091
ID ADF15091 standard; protein; 769 AA.
XX
AC ADF15091;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human albumin therapeutic fusion protein SeqID387.
XX
KW albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human.
XX
OS Chimeric.
OS Homo sapiens.
XX
PN W02003060071-A2.
XX
PD 24-JUL-2003.
XX
PF 23-DEC-2002; 2002WO-US040891.
XX
PR 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 28-JAN-2002; 2002US-0351360P.
PR 26-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-MAY-2002; 2002US-0382617P.
PR 28-MAY-2002; 2002US-0383123P.
PR 05-JUN-2002; 2002US-0385708P.
PR 10-JUL-2002; 2002US-0394625P.
PR 24-JUL-2002; 2002US-0398008P.
PR 09-AUG-2002; 2002US-0402131P.
PR 13-AUG-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 02-OCT-2002; 2002US-0411426P.
PR 11-OCT-2002; 2002US-0414984P.
PR 23-OCT-2002; 2002US-0417611P.
PR 05-NOV-2002; 2002US-0420246P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX (DELZ) DELTA BIOTECHNOLOGY LTD.
XX
XX (PRIN) PRINCIPIA PHARM CORP.
XX
PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX
XX WPI; 2003-598517/56.
XX
XX New albumin fusion protein, useful for preparing a composition for
XX treating diabetes mellitus.
PT

XX Example 4; SEQ ID NO 387; 24pp; English.

PS This invention relates to a novel albumin fusion protein having albumin

CC or biological activity. Human serum albumin is responsible for a

CC significant proportion of the osmotic pressure of serum and also

CC functions as a carrier of endogenous and exogenous ligands. The fusion of

CC albumin to a therapeutic protein may increase shelf-life and stability of

CC the therapeutic protein. The albumin fusion protein of the invention may

CC allow production of compositions with antidiabetic activity whilst the

CC nucleotide sequence which encodes it may be useful for gene therapy. The

CC albumin fusion protein is useful for preparing a composition for treating

CC diabetes mellitus. The present sequence is the amino acid sequence of a

CC novel full-length human albumin therapeutic fusion protein of the

CC invention. Note: The sequence data for this patent did not form part of

CC the printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/publishedpct_sequences

XX Sequence 769 AA;

SQ

Query Match 94.9%; Score 852; DB 7; Length 769;

Best Local Similarity 99.4%; Pred. No. 1.3e-83;

Matches 166; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 HYAPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQ 66

DB 18 HSAPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQ 77

QY 67 QAVEVWQGLALISEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLRLALGAKQA 126

DB 78 QAVEVWQGLALISEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLRLALGAKQA 137

QY 127 ISPPDAASAAPLRTITADTFKRLFRVYSNFLRGKLYTGACRTGD 173

DB 138 ISPPDAASAAPLRTITADTFKRLFRVYSNFLRGKLYTGACRTGD 184

RESULT 11

AAP70398

ID AAP70398 standard; protein; 166 AA.

XX

AC AAP70398;

XX

DT 19-FEB-1991 (first entry)

XX

DE Sequence of human erythropoietin (EPO).

XX

KW Mega-karyocyte-platelet growth factor; hormone;

KW mega-karyocyte colony stimulating factor; therapy;

KW small acetyl cholinesterase positive cell; erythrocyte growth effect.

XX

OS Homo sapiens.

XX

PN JP62149624-A.

XX

PD 03-JUL-1987.

XX

PF 15-AUG-1986; 86JP-00191542.

XX

PR 13-SEP-1985; 85JP-00203049.

XX

PA (KAWA/) KAWAKITA M.

XX

DR WPI; 1987-224837/32.

XX

PT Megakaryocyte-platelet growth factor - contains as active component human

PT erythropoietin and is used to treat diseases caused by decrease in

PT platelets.

XX

PS Disclosure; Page 181; 8pp; Japanese.

XX

CC All of the Cys residues in the SQ are labelled "SH". Megakaryocyte-

CC platelet growth factor contains human EPO as an active principle. Human

CC EPO has a megakaryocyte colony-stimulating activity and increases the

CC ratio of small acetyl cholinesterase positive cell (SACHE+) which is

CC immature megakaryocyte. Human EPO effects megakaryocyte-platelet system

CC other than an erythrocyte growth effect. Megakaryocyte-platelet growth is

CC useable as a remedy for diseases caused by a platelet decrease

XX

SQ Sequence 166 AA;

Query Match 94.8%; Score 851; DB 1; Length 166;

Best Local Similarity 100.0%; Pred. No. 1.9e-84;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 68

DB 1 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60

QY 69 VEYVWQGLALISEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLRLALGAKQAIS 128

DB 61 VEYVWQGLALISEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLRLALGAKQAIS 120

QY 129 PPDAASAAPLRTITADTFKRLFRVYSNFLRGKLYTGACRTGDR 174

DB 121 PPDAASAAPLRTITADTFKRLFRVYSNFLRGKLYTGACRTGDR 166

RESULT 12

AAR23593

ID AAR23593 standard; protein; 166 AA.

XX

AC AAR23593;

XX

DT 20-OCT-1992 (first entry)

XX

DE Recombinant hematopoietic molecule portion 2.

XX

KW Erythropoietin; EPO; erythrocytes; IL-3; haematopoiesis.

XX

OS Homo sapiens.

XX

PN W09206116-A.

XX

PD 16-APR-1992.

XX

PF 26-SEP-1991; 91WO-US007053.

XX

PR 28-SEP-1990; 90US-00589958.

XX

PA (ORTH) ORTHO PHARM CORP.

XX

PI Rosen JT;

XX

DR WPI; 1992-150819/18.

XX

PT Recombinant haematopoietic molecules useful in treating anaemia(s) -

PT comprise IL3 or GM-CSF and EPO, G-CSF, IL-5 or M-CSF and has early and

PT later myeloid differentiation activity.

XX

PS Disclosure; Page 32; 82pp; English.

XX

CC This protein sequence given comprises the entire amino acid sequence of

CC human erythropoietin (EPO). EPO leads to the maturation of erythrocytes

CC and is therefore designated as a late myeloid differentiation factor

CC (MDF). Within the scope of the invention hybrid molecules were produced

CC which contain at least a portion of an early MDF and at least a portion

CC of a late MDF covalently linked. The EPO sequence given is effective

CC within the scope of the invention in full or in a truncated version.

CC Amino acids 7-161 act as a late MDF when recombined with an early MDF eg.

CC IL-3. These compounds can be used to promote hematopoiesis in a patient.

CC The bonding of the early and late factors allows a very high conc. of

CC late MDF at the surface of a cell which the early MDF is bound. It also

CC allows the early MDA to act more specifically to stimulate only the

CC desired lineage, thus reducing undesirable effects. These compounds are

CC useful for treating anaemias of various origins eg. renal failure and

CC AIDS. It is easier to produce and administer one recombinant molecule
 CC rather than two separate molecules

XX SQ Sequence 166 AA;

Query Match 94.8%; Score 851; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.9e-84; Mismatches 0; Indels 0; Gaps 0;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 APPRLICDSRVLELYLLEAKAEENITTCGAHCSLNENITVPTKVFYAWKMEVGQQA 68
 DB 1 APPRLICDSRVLELYLLEAKAEENITTCGAHCSLNENITVPTKVFYAWKMEVGQQA 60
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVGSLRSLTLLRALGAQKEATS 128
 DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVGSLRSLTLLRALGAQKEATS 120
 QY 129 PPDAAASAPLRTITADTFKFLFRVYSNFRGLKLYTGACRTGDR 174
 DB 121 PPDAAASAPLRTITADTFKFLFRVYSNFRGLKLYTGACRTGDR 166

RESULT 13
 AAW58404
 ID AAW58404 standard; protein; 166 AA.

XX AC AAW58404;

XX DT 12-OCT-1998 (first entry)

XX DE Human erythropoietin.

XX KW Erythropoietin receptor agonist; EPO; human; anaemia;
 KW haematopoietic deficiency; red blood cell; erythroid progenitor;
 KW bone marrow suppression.

XX OS Homo sapiens.

XX PN W09818926-A1.

XX PD 07-MAY-1998.

XX PF 23-OCT-1997; 97WO-US018703.

XX PR 25-OCT-1996; 96US-0034044P.

XX PA (SEAR) SEARLE & CO G D.

XX PI McWharter CA, Feng Y, Summers N;

XX DR WPI; 1998-272221/24.

XX DR N-PSDB; AAV31031.

XX PT Human erythropoietin receptor agonist polypeptide - used to stimulate the
 PT production of red blood cells in a patient.

XX PS Claim 1; Page 93; 112pp; English.

XX A claimed human erythropoietin (EPO) receptor agonist polypeptide
 CC comprises a modified EPO amino acid sequence given in AAW58404, where (a)
 CC optionally 1-6 amino acids from the N-terminus and 1-5 from the C-
 CC terminus can be deleted, (b) the N-terminus is joined to the C-terminus
 CC directly or through a linker (see AAW58405-12) capable of joining the N-
 CC terminus to the C-terminus, (c) there are new C- and N-termini at any two
 CC consecutive amino acids from amino acids 23-24 to 38-39, 40-41 to 41-42,
 CC 43-44 to 48-49, 50-51 to 57-58, 77-78 to 82-83, 84-85 to 88-89, and 108-
 CC 109 to 131-132, and (d) optionally the agonist polypeptide is preceded by
 CC Met, Ala, or Met-Ala. 60 Of these circularly permuted EPO receptor
 CC agonists (see AAW58413-72) are claimed. Also claimed are: nucleic acid
 CC molecules (see AAV30971-V31030) encoding novel EPO receptor agonists; a
 CC method of producing an EPO receptor agonist using transformed or
 CC transfected host cells; and methods for stimulating the production of
 CC haematopoietic cells, for selective ex vivo expansion of erythroid

CC progenitors, and treating patients having a haematopoietic disorder using
 CC the EPO receptor agonists. The EPO receptor agonists retain one or more
 CC activities of native EPO and may also show improved haematopoietic cell-
 CC stimulating activity and/or an improved activity profile which may
 CC include reduction of undesirable biological activities associated with
 CC native EPO and/or have improved physical properties such as increased
 CC solubility, stability and refold efficiency

XX SQ Sequence 166 AA;

Query Match 94.8%; Score 851; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.9e-84; Mismatches 0; Indels 0; Gaps 0;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 APPRLICDSRVLELYLLEAKAEENITTCGAHCSLNENITVPTKVFYAWKMEVGQQA 68
 DB 1 APPRLICDSRVLELYLLEAKAEENITTCGAHCSLNENITVPTKVFYAWKMEVGQQA 60
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVGSLRSLTLLRALGAQKEATS 128
 DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVGSLRSLTLLRALGAQKEATS 120
 QY 129 PPDAAASAPLRTITADTFKFLFRVYSNFRGLKLYTGACRTGDR 174
 DB 121 PPDAAASAPLRTITADTFKFLFRVYSNFRGLKLYTGACRTGDR 166

RESULT 14
 AAW77780
 ID AAW77780 standard; protein; 166 AA.

XX AC AAW77780;

XX DT 24-NOV-1998 (first entry)

XX DE Human EPO receptor agonist polypeptide.

XX KW Haematopoietic receptor agonist; erythropoietin receptor agonist; EPO;
 KW human; chimeric protein; stem cell expansion; tumour; infection;
 KW autoimmune disease; haematopoietic disorder; therapy; dendritic cell.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT Misc-difference 1. .6
 FT /note= "1-6 amino acids of the N-terminus are optionally
 FT deleted"
 FT Misc-difference 23. .24
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 24. .25
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 25. .26
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 26. .27
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 27. .28
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 28. .29
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 29. .30
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 30. .31
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 31. .32
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 32. .33
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 33. .34
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 34. .35
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 35. .36
 FT /note= "possible positions of new C- and N-termini"

CC human flt-3 receptor agonist polypeptide (see AAW77782); (d) a modified
CC human granulocyte colony stimulating factor (G-CSF) polypeptide (see
CC AAW77783); (e) modified human interleukin-3 polypeptide (see AAW77784);
CC (f) modified human c-mpl ligand polypeptide (see AAW77785); and (g) a
CC factor selected from the group consisting of a CSF, a cytokine, a
CC lymphokine, an interleukin and a haematopoietic growth factor, provided
CC that at least R1 or R2 is selected from (a), (b) or (c) as above. The
CC multi-functional chimeric haematopoietic receptor agonist can be used to
CC stimulate the production of haematopoietic cells in a patient, for the ex
CC vivo expansion of haematopoietic cells, for the production of dendritic

Query Match 94.8%; Score 851; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.9e-84; Mismatches 0; Gaps 0;
Matches 166; Conservative 0; Indels 0;

QY 9 APPRLICDSRVLLERYLLEAKEAENITTCABHCSLNENITVPDTKVFYAKRMEVGQQA 68
DB 1 APPRLICDSRVLLERYLLEAKEAENITTCABHCSLNENITVPDTKVFYAKRMEVGQQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVVDKAVSGLRSLLTLLRALGAQKEAIS 128
DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVVDKAVSGLRSLLTLLRALGAQKEAIS 120
QY 129 PPDAASAAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 174
DB 121 PPDAASAAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166

RESULT 15
ABB07030
ID ABB07030 standard; protein; 166 AA.
AC ABB07030;
XX
DT 21-JUN-2002 (first entry)
XX
DE Modified erythropoietin related gene protein sequence.
XX
KW Modified erythropoietin; EPO.
XX
OS Unidentified.
XX
PN KR145802-B1.
XX
PD 01-AUG-1998.
XX
PF 31-MAY-1994; 94KR-00012082.
XX
PR 31-MAY-1994; 94KR-00012082.
XX
PA (GLDS) LG CHEM CO LTD.
XX
PI Kim C, Song Y, Lee T;
XX
DR WPI; 2000-234250/20.
XX
DR N-PSDB; ABL50878.
XX
PT MODIFIED ERYTHROPOIETIN GENE AND EXPRESSION VECTORS THEREOF.
XX
PS Disclosure; Page 14; 15pp; Korean.
XX
CC The present invention describes modified erythropoietin (EPO) genes and
CC expression vectors comprising the genes. The present sequence represents
CC a protein sequence from the present invention
XX
SQ Sequence 166 AA;

Query Match 94.8%; Score 851; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.9e-84; Mismatches 0; Gaps 0;
Matches 166; Conservative 0; Indels 0;
QY 9 APPRLICDSRVLLERYLLEAKEAENITTCABHCSLNENITVPDTKVFYAKRMEVGQQA 68
|||||

Db 1 APPRLICDSRVLLERYLLEAKEAENITTCABHCSLNENITVPDTKVFYAKRMEVGQQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVVDKAVSGLRSLLTLLRALGAQKEAIS 128
DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVVDKAVSGLRSLLTLLRALGAQKEAIS 120
QY 129 PPDAASAAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 174
DB 121 PPDAASAAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166
Search completed: November 19, 2004, 21:05:45
Job time : 62.2534 secs

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OM protein - protein search, using sw model

Run on: November 19, 2004, 21:00:09 ; Search time 17.8375 Seconds
(without alignments)
646.913 Million cell updates/sec

Title: US-10-014-363-5

Perfect score: 898

Sequence: 1 APPGAHAYAPRLICDSRLV.....NFLRGKLYTGACRTGDR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	94.8	166	1	US-08-318-193-70
2	851	94.8	166	3	US-09-604-871-2
3	851	94.8	166	4	US-09-604-938-2
4	851	94.8	166	4	US-09-462-941-2
5	851	94.8	166	5	PCT-US94-04361-37
6	851	94.8	193	1	US-07-903-220-1
7	851	94.8	193	2	US-08-883-795A-34
8	851	94.8	193	4	US-09-552-265B-4
9	848	94.4	412	4	US-09-366-009-34
10	848	94.4	412	4	US-08-809-156B-34
11	846	94.2	165	3	US-09-604-871-1
12	846	94.2	165	4	US-09-604-938-1
13	846	94.2	165	4	US-09-830-967-1
14	843	93.9	165	4	US-09-554-451-8
15	843	93.9	193	4	US-09-552-265B-2
16	839	93.4	193	4	US-09-552-265B-5
17	835	93.0	166	5	PCT-US94-04361-45
18	830	92.4	166	4	US-09-552-265B-30
19	830	92.4	193	4	US-09-552-265B-46
20	829	92.3	166	4	US-09-552-265B-22
21	829	92.3	166	4	US-09-552-265B-32
22	829	92.3	193	4	US-09-552-265B-38
23	829	92.3	193	4	US-09-552-265B-48
24	827	92.1	166	4	US-09-552-265B-20
25	827	92.1	166	4	US-09-552-265B-24
26	827	92.1	193	4	US-09-552-265B-36
27	827	92.1	193	4	US-09-552-265B-40

28 826 92.0 166 4 US-09-552-265B-26 Sequence 26, Appl
29 826 92.0 166 4 US-09-552-265B-31 Sequence 31, Appl
30 826 92.0 193 4 US-09-552-265B-42 Sequence 42, Appl
31 826 92.0 193 4 US-09-552-265B-47 Sequence 47, Appl
32 825 91.9 166 4 US-09-552-265B-18 Sequence 18, Appl
33 825 91.9 166 4 US-09-552-265B-23 Sequence 23, Appl
34 825 91.9 166 4 US-09-552-265B-28 Sequence 28, Appl
35 825 91.9 193 4 US-09-552-265B-33 Sequence 33, Appl
36 825 91.9 193 4 US-09-552-265B-39 Sequence 39, Appl
37 825 91.9 193 4 US-09-552-265B-44 Sequence 44, Appl
38 825 91.9 193 4 US-09-552-265B-49 Sequence 49, Appl
39 825 91.9 193 4 US-09-552-265B-21 Sequence 21, Appl
40 823 91.6 166 4 US-09-552-265B-25 Sequence 25, Appl
41 823 91.6 193 4 US-09-552-265B-37 Sequence 37, Appl
42 823 91.6 193 4 US-09-552-265B-41 Sequence 41, Appl
43 822 91.5 166 4 US-09-552-265B-27 Sequence 27, Appl
44 822 91.5 193 4 US-09-552-265B-43 Sequence 43, Appl
45

ALIGNMENTS

RESULT 1

US-08-318-193-70

; Sequence 70, Application US/08318193

; Patent No. 5641663

; GENERAL INFORMATION:

; APPLICANT: GARVIN, Robert T.

; APPLICANT: MALEK, Lawrence T.

; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION

; TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY

; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS

; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES

; NUMBER OF SEQUENCES: 91

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/318,193

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935,314

; FILING DATE:

; APPLICATION NUMBER: US 07/224,568

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 18740/116 CACO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)683-4109

; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 70:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 166 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-318-193-70

Query Match

Best Local Similarity 94.8%; Score 851; DB 1; Length 166;

Pred. No. 1.7e-98;

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; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-604-938-2

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	Query Match	94.9%	Score 851;	DB 4;	Length 166;
	Best Local Similarity	100.0%;	Pred. No. 1.7e-98;		
	Matches 166;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	9	APPLICDSRVLERYLLEAKEAENITTCGAHCSLNEINITVPDTKNFYAWKRMVEVQQA	68		
Db	1	APPLICDSRVLERYLLEAKEAENITTCGAHCSLNEINITVPDTKNFYAWKRMVEVQQA	60		
Qy	69	VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGNQKEAIS	128		
Db	61	VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGNQKEAIS	120		
Qy	129	PPDAASAAPTITADTFKLFVYSNFLRGKCLKLYTGEACRTGDR	174		
Db	121	PPDAASAAPTITADTFKLFVYSNFLRGKCLKLYTGEACRTGDR	166		

```

RESULT 4
US-09-462-941-2
; Sequence 2, Application US/09462941
; Patent No. 6608183
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/09/462,941
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-462-941-2

```

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Query Match      94.8%; Score 851; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.7e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      9 APPRLICDSRVLERVLLKAEKENITTCGAHCSSLNENITVPDTKVNFYAKRMEVGQQA 68
      |||||
Db      1 APPRLICDSRVLERVLLKAEKENITTCGAHCSSLNENITVPDTKVNFYAKRMEVGQQA 60

QY      69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHYDVKAVSGURSLTTLRLGAQKEALS 128
      |||||
Db      61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHYDVKAVSGURSLTTLRLGAQKEALS 120

QY      129 PDAASAAPLRITITADTRFKLFRVYSNFRGLKLYLTGEACRTGDR 174
      |||||
Db      121 PDAASAAPLRITITADTRFKLFRVYSNFRGLKLYLTGEACRTGDR 166

RESULT 5
PCT-US94-04361-37
; Sequence 37, Application PC/TUS9404361
; GENERAL INFORMATION:
; APPLICANT: Brigham and Women's Hospital
; APPLICANT: 75 Francis Street
; APPLICANT: Boston, MA 02115

```

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/07/903,220
; FILING DATE: 19920731
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: 1248/27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
US-07-903-220-1

Query Match 94.8%; Score 851; DB 1; Length 193;
Best Local Similarity 100.0%; Pred.No. 2.2e-98;
Matches 166; Conservative 0; Mismatches 0; Indels 0

QY 9 APRRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAKWKI
Db 28 APRRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAKWKI
QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLRLAL
Db 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLRLAL
QY 129 PPDAAAPLRTITADTFRKLFVYNSFLRGKLYTGACRTGDR 174
Db 148 PPDAAAPLRTITADTFRKLFVYNSFLRGKLYTGACRTGDR 193

RESULT 7
US-08-883-795A-34
; Sequence 34, Application US/08883795A
; Patent No. 5985607
; GENERAL INFORMATION:
; APPLICANT: Delcuvie, Genevieve
; APPLICANT: Awang, Gregor
; TITLE OF INVENTION: Recombinant DNA Molecules and Expression
; TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESS: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,795A
; FILING DATE: 27-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gravelle, Micheline
; REGISTRATION NUMBER: 40,261
; REFERENCE/DOCKET NUMBER: 7841-062

```

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 364-7311
 TELEFAX: (416) 361-1398
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 193 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-883-795A-34

Query Match 94.8%; Score 851; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 2.2e-98;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAKRMEVGQQA 68
 DB 28 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAKRMEVGQQA 87
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKAVSGLSRLTLLRALGAQKEAIS 128
 DB 88 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKAVSGLSRLTLLRALGAQKEAIS 147
 QY 129 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGACRTGDR 174
 DB 148 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGACRTGDR 193

RESULT 8

US-09-552-265B-4

Sequence 4, Application US/09552265B
 Patent No. 6555343
 GENERAL INFORMATION:
 APPLICANT: DeSavage, Frederick
 APPLICANT: Hennen, Dennis J.
 TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
 FILE REFERENCE: polypeptides and nucleic acids encoding the same
 CURRENT FILING DATE: 2000-04-19
 PRIOR FILING DATE: 1999-05-17
 NUMBER OF SEQ ID NOS: 49
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 193
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-552-265B-4

Query Match 94.8%; Score 851; DB 4; Length 193;
 Best Local Similarity 100.0%; Pred. No. 2.2e-98;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAKRMEVGQQA 68
 DB 28 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAKRMEVGQQA 87
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKAVSGLSRLTLLRALGAQKEAIS 128
 DB 88 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKAVSGLSRLTLLRALGAQKEAIS 147
 QY 129 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGACRTGDR 174
 DB 148 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGACRTGDR 193

RESULT 9

US-09-366-009-34

Sequence 34, Application US/09366009
 Patent No. 6426042
 GENERAL INFORMATION:
 APPLICANT: Asada, Kiyozo

Uemori, Takashi
 Ueno, Takashi
 Koyama, No. 6426042uto
 Hashino, Kimikazu
 Kato, Ikunoshin
 TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
 CELLS WITH RETROVIRUS
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WEISER & ASSOCIATES
 STREET: 230 South Fifteenth Street, Suite 500
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/366,009
 FILING DATE: 02-Aug-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/809,156
 FILING DATE: <Unknown>
 APPLICATION NUMBER: JP 294382/1995
 FILING DATE: 13-NOV-1995
 APPLICATION NUMBER: JP 051847/1996
 FILING DATE: 08-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Weiser, Gerard J.
 REGISTRATION NUMBER: 19,763
 REFERENCE/DOCKET NUMBER: 977.6507P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-875-8383
 TELEFAX: 215-875-8394
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 412 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 34:
 US-09-366-009-34

Query Match 94.4%; Score 848; DB 4; Length 412;
 Best Local Similarity 99.4%; Pred. No. 1.7e-97;
 Matches 165; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAKRMEVGQQA 68
 DB 233 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKYNFYAKRMEVGQQA 292
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKAVSGLSRLTLLRALGAQKEAIS 128
 DB 293 VEVWQGLALLSEAVLRGQALLVNSQWPWEPQLQHVDAKAVSGLSRLTLLRALGAQKEAIS 352
 QY 129 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGACRTGDR 174
 DB 353 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGACRTGDR 398

RESULT 10

US-08-809-156B-34

Sequence 34, Application US/08809156B
 Patent No. 6472204
 GENERAL INFORMATION:
 APPLICANT: Asada, Kiyozo
 APPLICANT: Uemori, Takashi
 APPLICANT: Ueno, Takashi

APPLICANT: Koyama, No. 6472204uto
 APPLICANT: Hashino, Kimikazu
 APPLICANT: Kato, Ikunoshin
 TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
 TITLE OF INVENTION: CELLS WITH RETROVIRUS
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WEISER & ASSOCIATES
 STREET: 230 South Fifteenth Street, Suite 500
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/809,156B
 FILING DATE: 07-MAR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP96/03254
 FILING DATE: 07-NOV-1996
 APPLICATION NUMBER: JP 294382/1995
 FILING DATE: 13-NOV-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 051847/1996
 FILING DATE: 08-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Weiser, Gerard J.
 REGISTRATION/DOCKET NUMBER: 19,763
 REFERENCE/DOCKET NUMBER: 977.6507P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-875-8383
 TELEFAX: 215-875-8394
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 412 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-809-156B-34

Query Match 94.4%; Score 848; DB 4; Length 412;
 Best Local Similarity 99.4%; Pred. No. 1.7e-97;
 Matches 165; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 9 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKRMVGGQQA 68
 Db 233 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKRMVGGQQA 292
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 128
 Db 293 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 352
 QY 129 PDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGDR 174
 Db 353 PDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGDR 398

RESULT 11
 US-09-604-871-1
 ; Sequence 1, Application US/09604871
 ; Patent No. 6340742
 ; GENERAL INFORMATION:
 ; APPLICANT: Burg, Josef
 ; APPLICANT: Hilger, Bernd
 ; APPLICANT: Josel, Hans-Peter
 ; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES

; FILE REFERENCE: 1098 nonprovisional
 ; CURRENT APPLICATION NUMBER: US/09/604,871
 ; CURRENT FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/151,454
 ; PRIOR FILING DATE: 1999-08-30
 ; PRIOR APPLICATION NUMBER: 60/147,452
 ; PRIOR FILING DATE: 1999-08-05
 ; PRIOR APPLICATION NUMBER: 60/142,243
 ; PRIOR FILING DATE: 1999-07-02
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 165
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-604-871-1

Query Match 94.2%; Score 846; DB 3; Length 165;
 Best Local Similarity 100.0%; Pred. No. 7.2e-98;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKRMVGGQQA 68
 Db 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKRMVGGQQA 60
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 128
 Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 120
 QY 129 PDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGD 173
 Db 121 PDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGD 165

RESULT 12
 US-09-604-938-1
 ; Sequence 1, Application US/09604938
 ; Patent No. 6583272
 ; GENERAL INFORMATION:
 ; APPLICANT: Bailon, Pascal
 ; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
 ; FILE REFERENCE: 1097 nonprovisional
 ; CURRENT APPLICATION NUMBER: US/09/604,938
 ; CURRENT FILING DATE: 2000-06-27
 ; PRIOR APPLICATION NUMBER: 60/166,151
 ; PRIOR FILING DATE: 1999-11-17
 ; PRIOR APPLICATION NUMBER: 60/151,548
 ; PRIOR FILING DATE: 1999-08-13
 ; PRIOR APPLICATION NUMBER: 60/150,225
 ; PRIOR FILING DATE: 1999-08-23
 ; PRIOR APPLICATION NUMBER: 60/142,254
 ; PRIOR FILING DATE: 1999-07-02
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 165
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-604-938-1

Query Match 94.2%; Score 846; DB 4; Length 165;
 Best Local Similarity 100.0%; Pred. No. 7.2e-98;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKRMVGGQQA 68
 Db 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAWKRMVGGQQA 60
 QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 128
 Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 120
 QY 129 PDAASAAPLRTITADTFKLFVYSNFRGKLYTGACRTGD 173

Db 121 PDAAASAPLRTITADTFKFLFRVSNFLRGKLYTGACRTGD 165

RESULT 13

US-09-830-967-1
; Sequence 1, Application US/09830967
; Patent No. 6777205
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie No. 6777205th America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Host Cells Expressing Recombinant Human Erythropoietin
; FILE REFERENCE: 1909.0020002
; CURRENT APPLICATION NUMBER: US/09/830,967
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: AR 99-01-00679
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: AR 98-01-05609
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-967-1

Query Match 94.2%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.2e-98; Indels 0; Gaps 0;
Matches 165; Conservative 0; Mismatches 0;
QY 9 APPRLICDSRVLELYLEAKEAENITTCGAHCNSLNENITVPDTKVNFYAKRMEVGGQA 68
Db 1 APPRLICDSRVLELYLEAKEAENITTCGAHCNSLNENITVPDTKVNFYAKRMEVGGQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
QY 129 PDAAASAPLRTITADTFKFLFRVSNFLRGKLYTGACRTGD 173
Db 121 PDAAASAPLRTITADTFKFLFRVSNFLRGKLYTGACRTGD 165

RESULT 14

US-09-554-451-8
; Sequence 8, Application US/09554451
; Patent No. 6680207
; GENERAL INFORMATION:
; APPLICANT: Jonathan Paul MURPHY
; APPLICANT: Anthony ATKINSON
; TITLE OF INVENTION: Detection of Molecules in Samples
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/554,451
; FILING DATE: 15-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB98/03449
; FILING DATE: NO. 6680207ember 16, 1998
; APPLICATION NUMBER: GB 9723955.2
; FILING DATE: NO. 6680207ember 14, 1997
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-554-451-8

Query Match 93.9%; Score 843; DB 4; Length 165;
Best Local Similarity 99.4%; Pred. No. 1.7e-97; Indels 0; Gaps 0;
Matches 164; Conservative 1; Mismatches 0;
QY 9 APPRLICDSRVLELYLEAKEAENITTCGAHCNSLNENITVPDTKVNFYAKRMEVGGQA 68
Db 1 APPRLICDSRVLELYLEAKEAENITTCGAHCNSLNENITVPDTKVNFYAKRMEVGGQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
QY 129 PDAAASAPLRTITADTFKFLFRVSNFLRGKLYTGACRTGD 173
Db 121 PDAAASAPLRTITADTFKFLFRVSNFLRGKLYTGACRTGD 165

RESULT 15

US-09-552-265B-2
; Sequence 2, Application US/09552265B
; Patent No. 6555343
; GENERAL INFORMATION:
; APPLICANT: Desauvage, Frederick
; APPLICANT: Henner, Dennis, J.
; TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
; TITLE OF INVENTION: polypeptides and nucleic acids encoding the same
; FILE REFERENCE: GENENT. 057CP1
; CURRENT APPLICATION NUMBER: US/09/552,265B
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: US 09/307307
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-09-552-265B-2

Query Match 93.9%; Score 843; DB 4; Length 193;
Best Local Similarity 99.4%; Pred. No. 2.2e-97; Indels 0; Gaps 0;
Matches 165; Conservative 0; Mismatches 1;
QY 9 APPRLICDSRVLELYLEAKEAENITTCGAHCNSLNENITVPDTKVNFYAKRMEVGGQA 68
Db 28 APPRLICDSRVLELYLEAKEAENITTCGAHCNSLNENITVPDTKVNFYAKRMEVGGQA 87
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
Db 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 147
QY 129 PDAAASAPLRTITADTFKFLFRVSNFLRGKLYTGACRTGD 174
Db 148 PDAAASAPLRTITADTFKFLFRVSNFLRGKLYTGACRTGD 193

Search completed: November 19, 2004, 21:13:03
Job time : 18.8375 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 21:11:10 ; Search time 82.4565 Seconds
(without alignments)
747.281 Million cell updates/sec

Title: US-10-014-363-5

Perfect score:

Sequence: 1 APPGAAHYAPPRLICDSRVL.....NFLRGKCLKLYTGEACRTGDR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs. 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

1

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications 22.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp:*
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- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pcp:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pcp:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pcp:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp:*
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- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pcp:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pcp:*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	898	100.0	174	13	US-10-014-363-5	Sequence 5, Appli	
2	861	95.9	174	13	US-10-014-363-3	Sequence 3, Appli	
3	856.5	95.4	169	13	US-10-014-363-4	Sequence 4, Appli	
4	851	94.8	166	9	US-09-853-731-2	Sequence 2, Appli	
5	851	94.8	166	13	US-10-014-363-2	Sequence 2, Appli	
6	851	94.8	166	14	US-10-241-356-2	Sequence 2, Appli	
7	851	94.8	166	14	US-10-293-551-2	Sequence 2, Appli	
8	851	94.8	166	14	US-10-400-377-2	Sequence 2, Appli	
9	851	94.8	166	14	US-10-400-708-2	Sequence 2, Appli	
10	851	94.8	166	14	US-10-298-148-2	Sequence 2, Appli	
11	851	94.8	166	15	US-10-360-101-227	Sequence 227, App	
12	851	94.8	166	15	US-10-467-115-1	Sequence 1, Appli	
13	851	94.8	166	16	US-10-658-834A-201	Sequence 201, App	

14	851	94.8	166	16	US-10-773-939-2	Sequence 2, Appl
15	851	94.8	166	16	US-10-774-149-2	Sequence 2, Appl
16	851	94.8	166	16	US-10-468-496-133	Sequence 133, App
17	851	94.8	166	17	US-10-773-654-2	Sequence 2, Appl
18	851	94.8	193	10	US-09-813-775C-4	Sequence 4, Appl
19	851	94.8	193	14	US-10-113-824-2	Sequence 2, Appl
20	851	94.8	193	16	US-10-612-665-10	Sequence 10, Appl
21	851	94.8	193	16	US-10-612-665-22	Sequence 22, Appl
22	851	94.8	193	16	US-10-612-665-112	Sequence 112, App
23	851	94.8	193	17	US-10-676-694-10	Sequence 10, Appl
24	851	94.8	193	17	US-10-676-694-22	Sequence 22, Appl
25	851	94.8	193	17	US-10-676-694-112	Sequence 112, App
26	851	94.8	428	14	US-10-435-608-10	Sequence 10, Appl
27	851	94.8	428	15	US-10-622-108-10	Sequence 10, Appl
28	849	94.5	166	16	US-10-658-834A-959	Sequence 959, App
29	849	94.5	166	16	US-10-658-834A-967	Sequence 967, App
30	849	94.5	425	14	US-10-435-608-8	Sequence 8, Appl
31	849	94.5	425	15	US-10-622-108-8	Sequence 8, Appl
32	848	94.4	166	16	US-10-658-834A-952	Sequence 952, App
33	848	94.4	166	16	US-10-658-834A-955	Sequence 955, App
34	848	94.4	166	16	US-10-658-834A-958	Sequence 958, App
35	848	94.4	166	16	US-10-658-834A-966	Sequence 966, App
36	848	94.4	193	14	US-10-435-608-4	Sequence 4, Appl
37	848	94.4	193	15	US-10-622-108-4	Sequence 4, Appl
38	848	94.4	193	16	US-10-612-665-63	Sequence 63, Appl
39	848	94.4	193	16	US-10-612-665-64	Sequence 64, Appl
40	848	94.4	193	16	US-10-612-665-70	Sequence 70, Appl
41	848	94.4	193	16	US-10-612-665-81	Sequence 81, Appl
42	848	94.4	193	16	US-10-612-665-88	Sequence 88, Appl
43	848	94.4	193	16	US-10-612-665-91	Sequence 91, Appl
44	848	94.4	193	17	US-10-676-694-63	Sequence 63, Appl
45	848	94.4	193	17	US-10-676-694-64	Sequence 64, Appl

ALIGNMENTS

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RESULT 1
US-10-014-363-5
; Sequence 5, Application US/10014363
; Publication No. US20020115833A1
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 174
; TYPE: PRT
; ORGANISM: CHO/dhfr-
US-10-014-363-5

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Db	61	RNEVGQQAQVEVMQGLALLSEAVLRGQALLVNSQPMPEPLQLHVDKAVSGLSRISUTTLRAL	120		

QY	121	GQAQKEAISPPDAAASAPLRTITADTFRKLFPRVYSNFLRGKLKYTGACRTGDR	174
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US-10-014-363-3			
; Sequence 3, Application US/10014363			
; Publication No. US20020115833A1			
; GENERAL INFORMATION:			
; APPLICANT: Burg, Josef			
; APPLICANT: Engel, Alfred			
; APPLICANT: Franze, Reinhard			
; APPLICANT: Hilger, Bernd			
; APPLICANT: Schurig, Hartmut Ernst			
; APPLICANT: Tischer, Wilhelm			
; APPLICANT: Wozny, Manfred			
; TITLE OF INVENTION: Erythropoietin Conjugates			
; FILE REFERENCE: Case 20805			
; CURRENT APPLICATION NUMBER: US/10/014,363			
; CURRENT FILING DATE: 2001-12-11			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 3			
; LENGTH: 174			
; TYPE: PRT			
; ORGANISM: CHO/dhfr-			
US-10-014-363-3			
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Best Local Similarity 97.1%; Pred. No. 1.7e-86;			
Matches 169; Conservative 0; Mismatches 5; Indels 0; Gaps 0			
QY	1	APPGAAYAPPRLICDSRVLYRLLLEAXEAEENITTCGAHCSLNENITVPDTKNFYAWK	60
DB	1	APPRIEGRAPRLICDSRVLSRYLLEAXEAEENITTCGAHCSLNENITVPDTKNFYAWK	60
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QY	121	GQAQKEAISPPDAAASAPLRTITADTFRKLFPRVYSNFLRGKLKYTGACRTGDR	174
DB	121	GQAQKEAISPPDAAASAPLRTITADTFRKLFPRVYSNFLRGKLKYTGACRTGDR	174
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US-10-014-363-4			
; Sequence 4, Application US/10014363			
; Publication No. US20020115833A1			
; GENERAL INFORMATION:			
; APPLICANT: Burg, Josef			
; APPLICANT: Engel, Alfred			
; APPLICANT: Franze, Reinhard			
; APPLICANT: Hilger, Bernd			
; APPLICANT: Schurig, Hartmut Ernst			
; APPLICANT: Tischer, Wilhelm			
; APPLICANT: Wozny, Manfred			
; TITLE OF INVENTION: Erythropoietin Conjugates			
; FILE REFERENCE: Case 20805			
; CURRENT APPLICATION NUMBER: US/10/014,363			
; CURRENT FILING DATE: 2001-12-11			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 4			
; LENGTH: 169			
; TYPE: PRT			
; ORGANISM: CHO/dhfr-			
US-10-014-363-4			
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Best Local Similarity 97.1%; Pred. No. 5.1e-86;			
Matches 149; Conservative 0; Mismatches 5; Indels 5; Gaps 5			

US-10-014-363-2

Query Match 94.8%; Score 851; DB 13; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVGQQA 68
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QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 129 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 174
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 166

RESULT 6

US-10-241-356-2
; Sequence 2, Application US/10241356
; Publication No. US2003007753A1
; GENERAL INFORMATION:
; APPLICANT: TISCHER, WILHELM
; TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
; FILE REFERENCE: 20971
; CURRENT APPLICATION NUMBER: US/10/241,356
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: EP 01122555.4
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-241-356-2

Query Match 94.8%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 129 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 174
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 166

RESULT 7

US-10-293-551-2
; Sequence 2, Application US/10293551
; Publication No. US20030120045A1
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/10/293,551
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/09/604,938
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225

; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-551-2

Query Match 94.8%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 129 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 174
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 166

RESULT 8

US-10-400-377-2
; Sequence 2, Application US/10400377
; Publication No. US20030162949A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,377
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-377-2

Query Match 94.8%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVGQQA 68
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVGQQA 60
QY 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 129 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 174
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGDR 166

RESULT 9

US-10-400-708-2
; Sequence 2, Application US/10400708
; Publication No. US20030166865A1
; GENERAL INFORMATION:

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; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,708
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-708-2

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Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 APRRLICDSRVLYRLLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAWKMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 129 PPDAASAAPLRTITADTFKFLFRVYNSFLRGKLYTGACRTGDR 174
Db 121 PPDAASAAPLRTITADTFKFLFRVYNSFLRGKLYTGACRTGDR 166

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US-10-298-148-2
; Sequence 2, Application US/10298148
; Publication No. US20030171284A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/298,148
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-148-2

Query Match          94.8%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYRLLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAWKMEVGGQA 68
Db 1 APRRLICDSRVLYRLLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAWKMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 129 PPDAASAAPLRTITADTFKFLFRVYNSFLRGKLYTGACRTGDR 174
Db 121 PPDAASAAPLRTITADTFKFLFRVYNSFLRGKLYTGACRTGDR 166

; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/298,148
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-708-2

Query Match          94.8%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYRLLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAWKMEVGGQA 68
Db 1 APRRLICDSRVLYRLLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAWKMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 129 PPDAASAAPLRTITADTFKFLFRVYNSFLRGKLYTGACRTGDR 174
Db 121 PPDAASAAPLRTITADTFKFLFRVYNSFLRGKLYTGACRTGDR 166

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RESULT 11
US-10-360-101-227
; Sequence 1, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 227
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of erythropoietin
US-10-360-101-227

Query Match          94.8%; Score 851; DB 15; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APRRLICDSRVLYRLLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAWKMEVGGQA 68
Db 1 APRRLICDSRVLYRLLLEAKAEENITTCAGHCSLNENITVPDTKYNFYAWKMEVGGQA 60

QY 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 129 PPDAASAAPLRTITADTFKFLFRVYNSFLRGKLYTGACRTGDR 174
Db 121 PPDAASAAPLRTITADTFKFLFRVYNSFLRGKLYTGACRTGDR 166

RESULT 12
US-10-467-115-1
; Sequence 1, Application US/10467115
; Publication No. US20040063917A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; TITLE OF INVENTION: MODIFIED ERYTHROPOIETIN (EPO) WITH
; FILE REFERENCE: MER-114
; CURRENT APPLICATION NUMBER: US/10/467,115
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: 01102615.0
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01174
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-467-115-1

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Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
US-10-773-939-2
; Sequence 2, Application US/10773939
; Publication No. US20040175356A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/773,939
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/10/400,377

Query Match	94.8%;	Score 851;	DB 16;	Length 166;
Best Local Similarity	100.0%;	Pred. No. 2e-85;		
Matches 166;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	9	APPRLICDSRVLERVLLFAKEAENITTTGCAEHCSLNENITVPD	T	TKNFYAWKMEVGGQA 68
dbb	1	APPRLICDSRVLERVLLFAKEAENITTTGCAEHCSLNENITVPD	T	TKNFYAWKMEVGGQA 60
QY	69	VEVMQGLALLSEAVLRGGQALLVNSSQPWEPLQJLHV	D	KAVSGLSRLTLLRALGCAQKEAIS 128
dbb	61	VEVMQGLALLSEAVLRGGQALLVNSSQPWEPLQJLHV	D	KAVSGLSRLTLLRALGCAQKEAIS 120
QY	129	PPDAASAAPLRTITADTFRKLPVYVSNFLRGKLLKYTG	E	ACRTGDR 174
dbb	121	PPDAASAAPLRTITADTFRKLPVYVSNFLRGKLLKYTG	E	ACRTGDR 166

Search completed: November 19, 2004, 21:32:15

Job time : 83.4565 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 20:59:24 ; Search time 20.1934 Seconds
(without alignments)
829.068 Million cell updates/sec

Title: US-10-014-363-5

Perfect score: 898

Sequence: 1 APPGAHYAPPRLICDSRVL.....NFLRGKLYTGEACRTGDR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	851	94.8	193	1	ZUHU	erythropoietin pre
2	770.5	85.8	132	1	TQ0173	erythropoietin pre
3	765.5	85.2	132	1	I84613	erythropoietin pre
4	718	80.0	188	1	I46083	erythropoietin pre
5	706	78.6	192	1	S28148	erythropoietin pre
6	690.5	76.9	194	1	I46401	erythropoietin pre
7	686	76.4	192	1	A24902	erythropoietin pre
8	685.5	76.3	195	2	JC7699	erythropoietin pre
9	683	76.1	190	2	I46578	erythropoietin - r
10	638	71.0	175	2	I46199	erythropoietin - p
11	90	10.0	353	2	G02729	erythropoietin - d
12	89	9.9	353	2	I80105	thrombopoietin - h
13	88	9.8	323	2	AB0323	thrombopoietin pre
14	87.5	9.7	346	2	AE0959	ribonucleoside-dip
15	86	9.6	286	2	A55330	Solute binding rec
16	85	9.5	339	2	AB3374	megakaryocyte grow
17	83.5	9.3	296	2	AI0443	UDP-N-acetylpyruvo
18	80.5	9.0	3033	1	GNWVJ8	probable 2-hydroxy
19	79.5	8.9	154	2	H82810	genome polypeptide
20	79.5	8.9	567	2	T08405	bacterioferritin x
21	79.5	8.9	741	2	D75500	hypothetical prote
22	79.5	8.9	1839	2	T35681	ATP-dependent Clp
23	79	8.8	480	2	S56639	probable sensory h
24	78.5	8.7	348	2	T35450	ribosomal protein
25	78.5	8.7	813	2	AF0526	ABC transporter AT
26	78.5	8.7	897	2	AF4696	ATP-dependent heli
27	78	8.7	455	2	AG2919	EGF receptor subet
28	78	8.7	455	2	H97693	conserved hypothet
29	78	8.7	747	1	S36741	methylamine utiliz
						probable copper-tr

30	77.5	8.6	242	2	AD1928	hypothetical prote
31	77	8.6	451	2	S75569	hypothetical prote
32	77	8.6	548	2	B84932	60 kD chaperonin [
33	77	8.6	548	2	B42281	symbionin symL - p
34	76.5	8.5	425	2	AE3465	mandelate racemase
35	75.5	8.4	544	2	S37039	groEL protein - Ba
36	75.5	8.4	637	2	S75772	hypothetical prote
37	74.5	8.3	400	2	AB2922	conserved hypothet
38	74.5	8.3	425	2	C97696	rts beta (AF305057
39	74.5	8.3	824	2	D64738	ATP-dependent heli
40	74	8.2	282	2	B37994	RF2 protein - sail
41	74	8.2	326	2	JC4125	thrombopoietin pre
42	74	8.2	335	2	AH3625	ribonucleoside-dip
43	74	8.2	347	2	A75537	hypothetical prote
44	74	8.2	544	2	B82048	chaperonin, 60 kD
45	74	8.2	552	2	S39765	chaperonin 60 - Co

ALIGNMENTS

RESULT 1

ZUHU

erythropoietin precursor [validated] - human

C:Species: Homo sapiens (man)

C:Date: 27-Nov-1985 #sequence revision 27-Nov-1985 #text_change 09-Jul-2004

C:Accession: A01855; A24744; A25384; A22210; S56178

R:Jacobs, K.; Shoemaker, C.; Rudersdorf, R.; Neill, S.D.; Kaufman, R.J.; Mufson, A.; See Nature 313, 806-810, 1985

A:Title: Isolation and characterization of genomic and cDNA clones of human erythropoiet

A:Reference number: A01855; MUID:85137899; PMID:3838366

A:Accession: A01855

A:Molecule type: mRNA; DNA

A:Residues: 1-193 <JAC>

A:Cross-references: UNIPROT:P01588; GB:X02157; GB:X02158

R:Lin, F.K.; Suggs, S.; Lin, C.H.; Browne, J.K.; Smalling, R.; Egrie, J.C.; Chen, K.K.; Proc. Natl. Acad. Sci. U.S.A. 82, 7580-7584, 1985

A:Title: Cloning and expression of the human erythropoietin gene.

A:Reference number: A24744; MUID:86067948; PMID:3865178

A:Accession: A24744

A:Molecule type: DNA

A:Residues: 1-193 <LIN>

A:Cross-references: GB:M11319; NID:gi82197; PIDN:AA52400.1; PID:gi82198

R:Iai, P.H.; Everett, R.; Wang, F.F.; Arakawa, T.; Goldwasser, E. J. Biol. Chem. 261, 3116-3121, 1986

A:Title: Structural characterization of human erythropoietin.

A:Reference number: A25384; MUID:86140080; PMID:3949763

A:Accession: A25384

A:Molecule type: protein

A:Residues: 28-86, 'Q', 87-193 <IAI>

A:Experimental source: urine

A:Note: Forms without the carboxyl-terminal residue and the four carboxyl-terminal resid

R:Yanagawa, S.; Hirade, K.; Ohnata, H.; Sasaki, R.; Chiba, H.; Ueda, M.; Goto, M. J. Biol. Chem. 259, 2707-2710, 1984

A:Title: Isolation of human erythropoietin with monoclonal antibodies.

A:Reference number: A22210; MUID:84135751; PMID:6698989

A:Accession: A22210

A:Molecule type: protein

A:Residues: 28-29, 'X', 31-33, 'I', 35-50, 'X', 52-53, 'D', 55, 'G', 57 <YAN>

R:Matsumoto, S.; Ikura, K.; Ueda, M.; Sasaki, R. Plant Mol. Biol. 27, 1163-1172, 1995

A:Title: Characterization of a human glycoprotein (erythropoietin) produced in cultured

A:Reference number: S56178; MUID:95284365; PMID:7766897

A:Accession: S56178

A:Molecule type: protein

A:Residues: 28-33, 'X', 35-37 <MTS>

C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o

A:Gene: GDB:EPO

A:Cross-references: GDB:119110; OMIM:133170

A:Map position: 7q21.3-7q22.1

A:Introns: 5/1; 53/3; 82/3; 142/3

C:Function:

A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-193/Product: erythropoietin #status experimental
F;34-188,56-60/Disulfide bonds: #status experimental
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;153/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 94.8%; Score 851; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFKVYAKRMEVQQA 68
DB 28 APPRLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFKVYAKRMEVQQA 87

QY 69 VEVQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 128
DB 88 VEVQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 147

QY 129 PPDAAAPLRTITADTFKRLFRVYNSFLRGKLYTGEACRTGDR 174
DB 148 PPDAAAPLRTITADTFKRLFRVYNSFLRGKLYTGEACRTGDR 193

RESULT 2
JQ0173
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 07-Sep-1990 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: JQ0173
R;Lin, F.K.; Lin, C.H.; Lai, P.H.; Browne, J.K.; Egrie, J.C.; Smalling, R.; Fox, G.M.; Q
Gene 44, 201-209, 1986
A;Title: Monkey erythropoietin gene: cloning, expression and comparison with the human e
A;Reference number: JQ0173; MUID:87055236; PMID:2877922
A;Accession: JQ0173
A;Molecule type: mRNA
A;Residues: 1-192 <LIN>
A;Cross-references: UNIPROT:P07865; GB:M18189; GB:M15819; GB:M18188; NID:g342
A;Experimental source: kidney
C;Comment: This protein is the principal hormone involved in the regulation of erythrocy
C;Function: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Superfamily: the primary inducer of erythrocyte formation
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-193/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;153/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 85.8%; Score 770.5; DB 1; Length 192;
Best Local Similarity 89.5%; Pred. No. 7.5e-66;
Matches 154; Conservative 7; Mismatches 6; Indels 5; Gaps 2;

QY 3 PGAAHYAPRLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFKVYAKR 62
DB 26 PG----APRLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFKVYAKR 81

QY 63 EVGQQAQVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTTLRALGA 122
DB 82 EVGQQAQVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTTLRALGA 141

QY 123 QKEAISPPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYTGEACRTGDR 174
DB 142 Q-EAISLPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYTGEACRTGDR 192

RESULT 3
I84613
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 02-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: I84613
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I84613
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-188 <WEN>
A;Cross-references: UNIPROT:P33708; GB:L10606; NID:gl63820; PIDN:AAA30807.1; PID:g16382
A;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver c
C;Function: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-188/Product: erythropoietin #status predicted <MAT>
F;29-183,51-55/Disulfide bonds: #status predicted
F;46,60,105/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 80.0%; Score 718; DB 1; Length 188;
Best Local Similarity 84.3%; Pred. No. 7.2e-61;
Matches 140; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFKVYAKRMEVQQA 68
DB 23 APPRLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFKVYAKRMEVQQA 82

C;Species: Macaca mulatta (rhesus macaque)
C;Date: 02-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: I84613
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I84613
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-192 <RES>
A;Cross-references: UNIPROT:Q28513; GB:L10609; NID:g342095; PIDN:AAA36842.1; PID:g342096
A;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver c
C;Function: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-193/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 85.2%; Score 765.5; DB 1; Length 192;
Best Local Similarity 88.4%; Pred. No. 2.2e-65;
Matches 152; Conservative 9; Mismatches 6; Indels 5; Gaps 2;

QY 3 PGAAHYAPRLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFKVYAKR 62
DB 26 PG----APRLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFKVYAKR 81

QY 63 EVGQQAQVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTTLRALGA 122
DB 82 EVGQQAQVEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTTLRALGA 141

QY 123 QKEAISPPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYTGEACRTGDR 174
DB 142 Q-EAISLPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYTGEACRTGDR 192

RESULT 4
I46083
C;Species: Felis silvestris catus (domestic cat)
C;Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: I46083
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I46083
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-188 <WEN>
A;Cross-references: UNIPROT:P33708; GB:L10606; NID:gl63820; PIDN:AAA30807.1; PID:g16382
A;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver c
C;Function: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-188/Product: erythropoietin #status predicted <MAT>
F;29-183,51-55/Disulfide bonds: #status predicted
F;46,60,105/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 80.0%; Score 718; DB 1; Length 188;
Best Local Similarity 84.3%; Pred. No. 7.2e-61;
Matches 140; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 9 APPRLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFKVYAKRMEVQQA 68
DB 23 APPRLICDSRVLYRLLYLLAEAEENITTCGAHCSLNENITVPDTKVNFKVYAKRMEVQQA 82

erythropoietin precursor - sheep
 I46401
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
 C:Accession: I46401; I47077
 R:Fu, P.; Evans, B.; Lim, G. B.; Moritz, K.; Wintour, E.M.
 Mol. Cell. Endocrinol. 93, 107-116, 1993
 A:Title: The sheep erythropoietin gene: molecular cloning and effect of hemorrhage on pl
 A:Reference number: I46401; MUID:93351736; PMID:8349021
 A:Accession: I46401
 A>Status: translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA

F;50,64,109/Binding site: carbohydrate

F;50,64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	76.1%	Score 683	DB 2	Length 190
Best Local Similarity	82.1%	Pred. No. 1.5e-57		
Matches 136	Conservative	7	Mismatches 21	Indels 2
Gaps				
QY	9	APPLICDSRVLYRLLEAKAEANITTCGAHCSLNENITVPDTKVNFWYAKRMEVGOQA	68	
DB	23	APPLICDSRVLYRLLEAKAEANITTCGAHCSLNENITVPDTKVNFWYAKRMEVGOQA	82	
QY	69	VEVWQGLALLSEAVLRQALLVNSSPQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS	128	
DB	83	MEVWQGLALLSEAVLRQALLVNSSPQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAIP	142	
QY	129	PPDA--ASAAPLRTITADTFKPLFRVYSNFLRGKLYGTGACRTGDR	174	
DB	143	LPDASPSAPLRTITADTFKPLFRVYSNFLRGKLYGTGACRRDR	190	
RESULT 10				
I46199				
erythropoietin - dog (fragment)				
C:Species: Canis lupus familiaris (dog)				
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004				
C:Accession: I46199				
R:Wen, D.; Boissel, J.				
Blood 82, 1507-1516, 1993				
A:Title: Erythropoietin structure-function relationships: High degree of sequence				
A:Reference number: I46083; MUID:93372347; PMID:8364201				
A:Accession: I46199				
A>Status: preliminary; translated from GB/EMBL/DBJ				
A:Molecule type: mRNA				
A:Residues: 1-175 <MEN>				
A:Cross-references: UNIPROT:P33707; GB:L13027; NID:g290087; PIDN:AAA30842.1; F				
C:Superfamily: erythropoietin				
Query Match	71.0%	Score 638	DB 2	Length 175
Best Local Similarity	81.0%	Pred. No. 2.7e-53		
Matches 124	Conservative	13	Mismatches 16	Indels 0
Gaps				
QY	9	APPLICDSRVLYRLLEAKAEANITTCGAHCSLNENITVPDTKVNFWYAKRMEVGOQA	68	
DB	23	APPLICDSRVLYRLLEAKAEANITTCGAHCSLNENITVPDTKVNFWYAKRMEVGOQA	82	
QY	69	VEVWQGLALLSEAVLRQALLVNSSPQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS	128	
DB	83	LEVWQGLALLSEAVLRQALLVNSSPQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAMS	142	
QY	129	PPDAASAAPLRTITADTFKPLFRVYSNFLRGKL	161	
DB	143	LPBEASAPLRTITADTFKPLFRVYSNFLRGKL	175	
RESULT 11				
G02729				
thrombopoietin - human				
C:Species: Homo sapiens (man)				
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999				
C:Accession: G02729				
R:im, S.				
submitted to the EMBL Data Library, May 1996				
A:Reference number: H01637				
A:Accession: G02729				
A>Status: preliminary; translated from GB/EMBL/DBJ				
A:Molecule type: mRNA				
A:Residues: 1-353 <IM>				
A:Cross-references: EMBL:U59493; NID:gl401245; PIDN:AAB03392.1; PID:gl401246				
C:Genetics:				
A:Gene: hTPO				
Query Match	10.0%	Score 90	DB 2	Length 353
Best Local Similarity	26.3%	Pred. No. 0.81		
Matches 41	Conservative	20	Mismatches 75	Indels 20
Gaps				

A;Cross-references: GDB:374007; OMIM:600044
A;Map position: 3q26.3-3q27
A;Introns: 5/1; 47/3; 76/3; 132/3
C;Keywords: alternative splicing; cytokine; glycoprotein

Query Match 9.9%; Score 89; DB 2; Length 353;
Best Local Similarity 26.3%; Pred. No. 1;
Matches 41; Conservative 20; Mismatches 75; Indels 20; Gaps 5;

QY 9 APPRLICDSRVLERYLLEAKEANITTCGAHCSLNENITVPTKYNFYAKRMEVGQQA 68
||| ||| : : : : : : : : : : : : : : : :
Db 24 APP--ACDLRVLSKLKRDSDVLHSRLSQCEVHEPLTPVLLPAVDPSLGEWKTQMETKA 81
||| ||| : : : : : : : : : : : : : : : :
QY 69 VEVWQGLALLSEAVL--RGQALLVNSSQPWEPLQLHVDKXAVSGLRISLTILLRALGAKKEA 126
:: : : : : : : : : : : : : : : :
Db 82 QDILGATVLLLEGVMARAGQGFTCLSLIGUGSQGVRLLEGALQSL-----LGTQ--- 132
||| ||| : : : : : : : : : : : : : : : :
QY 127 ISPPDAASAAPLRTITADTFRKLFVRYSNFKLK 162
||| ||| : : : : : : : : : : : : : : : :
Db 133 -LPQG-----RTTAHKDPNAIFLSFQHLLRKVR 161
||| ||| : : : : : : : : : : : : : : : :

RESULT 13
AB0323
ribonucleoside-diphosphate reductase (EC 1.17.4.1) beta chain [imported] - Versinia pestis
C;Species: Versinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0323
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentiss,
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan,
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Ewing,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Versinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-323 <CUR>
A;Cross-references: UNIPROT:Q8ZDC8; GB:AL590842; PIDN:CAC92889.1; PID:gl5980631;
C;Genetics:
A;Gene: nrdf
C;Superfamily: ribonucleoside-diphosphate reductase beta
C;Keywords: oxidoreductase

Query Match 9.8%; Score 88; DB 2; Length 323;
Best Local Similarity 25.2%; Pred. No. 1.1;
Matches 34; Conservative 20; Mismatches 59; Indels 22; Gaps 5;

QY 46 NITVPTKYNFYAKRMEVGQQADEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVD- 104
: : : : : : : : : : : : : : : :
Db 2 NVVKPTRISAINWNKIE-DDKDLEWN--RUTSFWLPEKVPGLNDIPSWSATLTPHEQQ 58
||| ||| : : : : : : : : : : : : : : : :
QY 105 ---KAVSGLSRLTTLRLAQ---KEAISPPDAASAPLRTITADTFRKLFVRYSNFNR 158
: : : : : : : : : : : : : : : :
Db 59 LTRIVETGTLTDITQNTLGA PALIKDAITPHEEAIFSNI SPWEAVHARSYSISFL-- 116
||| ||| : : : : : : : : : : : : : : : :
QY 159 GKLYTGCACTGD 173
||| ||| : : : : : : : : : : : : : : : :
Db 117 -----CLTSD 121
||| ||| : : : : : : : : : : : : : : : :

RESULT 14
AB0959
Solute binding receptor protein [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0959
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Croucher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.;
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Croucher,

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AE0959
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-346 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03169.1; PID:g16504804; GSPDB:GN00176
C:Genetics:
A:Gene: STY3952

Query Match 9.7%; Score 87.5; DB 2; Length 346;
Best Local Similarity 26.7%; Pred. No. 1.4;
Matches 44; Conservative 22; Mismatches 48; Indels 51; Gaps 9;
QY 18 RVLERYLLAKEAENITTG--CAEHCSLNE--NITVPDTKKNFYAKRMEVGQQAWEVWQ 73
DB 217 RNLQEMLERHPDANVAGSAIAEAAMGEGRNLTPLTIVSFYL-----THQVYR 267
QY 74 GLALLSEAVLRGOALLVNSQ--PWEPLQLHVDKAVGSLRSLTTLRALGAQ--KEAISPP 130
DB 268 GLK-----RGHILMALSQMAWQ-----GELAITOSIKVLQGPVPEINISPP 309
QY 131 -----DAASAAPLRTITADTFKLFPRVYSNLFRLGKLYTGEA 168
DB 310 VLILTHNNADSARVRSLSPPGFRPVY-----LYQYTSEA 344

RESULT 15
A55530
megakaryocyte growth and development factor, long form - human
N:Alternate names: MPL ligand, long form
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C:Accession: A55530
R:Chang, M.; McNinch, J.; Basu, R.; Shutter, J.; Hau, R.; Perkins, C.; Mar, V.; Suggs, S
J. Biol. Chem. 270, 511-514, 1995
A:Title: Cloning and characterization of the human megakaryocyte growth and development
A:Reference number: A55530; MUID:95122483; PMID:7822271
A:Accession: A55530
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-286 <CHA>
A:Cross-references: GB:U17071
C:Genetics:
A:Gene: MGDF
A:Map position: 3q26.3
C:Keywords: alternative splicing; cytokine

Query Match 9.6%; Score 86; DB 2; Length 286;
Best Local Similarity 26.6%; Pred. No. 1.5;
Matches 41; Conservative 18; Mismatches 75; Indels 20; Gaps 5;
QY 9 APPRLICDSRVLYRYLLEAKAEENITTCBAEHCSLNEITVPDTKKNFYAKRMEVGQQA 68
DB 24 APP--ACDLRVLSKLLRDSHVLSKLSQCPVHPPLTPVLLPAVDVDFSLGEMKTMQETKA 81
QY 69 VEVWQGLALLSEAVL--RGQALLVNSQSPWEPLQLHVDKAVGSLRSLTTLRALGAQKEA 126
DB 82 QDILGAVTLLLEGVMAARGQLGPTCLSLGQLSGQVRLILGALQSL-----LGTO--- 132
QY 127 ISPPDAASAAPLRTITADTFKLFPRVYSNLFRLGK 160
DB 133 -LPPQG-----RTAHKDPNAPILSFQHLRKG 159

Search completed: November 19, 2004, 21:12:05
Job time : 21.1934 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 20:59:03 ; Search time 103.996 Seconds
(without alignments)
962.682 Million cell updates/sec

Title: US-10-014-363-5

Perfect score: 898

Sequence: 1 APPGAHYAPPRLLCDRLV.....NFLRGKLYTGACRTGDR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Uniprot 02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	94.8	193	1	EPO HUMAN
2	851	94.8	193	2	AAP22357
3	770.5	85.8	192	1	EPO MACFA
4	765.5	85.2	192	1	EPO MACMU
5	728	81.1	192	2	Q867B1
6	711	79.2	192	1	EPO FELCA
7	706	78.6	192	1	EPO RAT
8	698	77.7	206	2	Q6PWU5
9	698	77.7	206	2	AAS77874
10	697.5	77.7	192	1	EPO BOVIN
11	694	77.3	192	1	EPO MOUSE
12	690.5	76.9	194	1	EPO SHEEP
13	685.5	76.3	195	2	Q9GKA2
14	685.5	76.3	195	2	Q9GKA3
15	683	76.1	190	1	EPO_PIG
16	683	76.1	192	2	Q6H8S9
17	683	76.1	192	2	Q6H8T0
18	683	76.1	192	2	Q6H8T1
19	683	76.1	194	2	Q9MYM8
20	679	75.6	192	2	Q6H8T2
21	663	73.8	133	2	Q8H288
22	658	73.3	133	2	Q8H289
23	638	71.0	175	1	EPO CANFA
24	627	69.8	131	2	Q8H287
25	607	67.6	133	2	Q8H286
26	554	61.7	133	2	Q8H285
27	241	26.8	195	2	Q6UAM1
28	241	26.8	195	2	AAR25698
29	238	26.5	182	2	Q6JV23
30	238	26.5	182	2	AAQ72466
31	238	26.5	185	2	Q6JV22

32	238	26.5	185	2	AAQ72467
33	188	20.9	50	2	Q9QV40
34	118	13.1	177	2	Q6IYE9
35	109	12.1	352	1	TPO CANFA
36	89	9.9	353	1	TPO HUMAN
37	88	9.8	333	2	Q8ZFC8
38	88	9.8	323	2	AAS62651
39	87.5	9.7	346	2	Q8Z2M5
40	87.5	9.7	346	2	Q8Z2K4
41	87.5	9.7	432	2	Q7QDZ2
42	85.5	9.5	154	2	Q87AY9
43	85	9.5	339	1	MURB PSEAE
44	85	9.5	861	2	Q8JEG9
45	85	9.5	3722	2	P94873

AaQ72467 fugu rubr
Q9qv40 rattus sp.
Q6IYE9 gallus gall
P42705 canis famil
P40225 homo sapien
Q8ZFC8 yersinia pe
AAS62651 yersinia
Q8Z2M5 salmonella
Q8Z2K4 salmonella
Q7QDZ2 anopheles g
Q87AY9 xylella fas
Q9hzm7 pseudomonas
Q8JEG9 human immun
P94873 lysobacter

ALIGNMENTS

RESULT 1

ID	EPO HUMAN	STANDARD;	PRT;	193 AA.
AC	P01588; Q9UDZ0; Q9UEZ5; Q9URAO;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Erythropoietin precursor (Epoetin).			
GN	Name=EPO;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85137899; PubMed=3838366;			
RA	Jacobs K., Shoemaker C., Rudersdorf R., Weill S.D., Kaufman R.J.,			
RA	Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F.,			
RA	Kawakita M., Shimizu T., Miyake T.,			
RT	"Isolation and characterization of genomic and cDNA clones of human			
RT	erythropoietin.";			
RL	Nature 313:806-810(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86067948; PubMed=3865178;			
RA	Lin F.-X., Suggs S., Lin C.-H., Browne J.K., Smalling R., Egrie J.C.,			
RA	Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai P.-H.,			
RA	Goldwasser E.;			
RT	"Cloning and expression of the human erythropoietin gene.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99018118; PubMed=9799793;			
RA	Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,			
RA	Tsu L.-C., Rosenthal A.;			
RT	"Large-scale sequencing of two regions in human chromosome 7q22:			
RT	analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci			
RT	reveals 17 genes.";			
RL	Genome Res. 8:1060-1073(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	Rupert J.L., Hochachka P.W.;			
RT	"Erythropoietin gene sequence in the Quechua, a high altitude native			
RT	population.";			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 58-193 FROM N.A., AND VARIANTS HEPATOCELLULAR CARCINOMA			
RP	131-ASN-PHE-132 AND GIN-149.			
RX	MEDLINE=93384593; PubMed=8396923;			
RA	Funakoshi A., Muta H., Baba T., Shimizu S.;			
RT	"Gene expression of mutant erythropoietin in hepatocellular			
RT	carcinoma.";			
RL	Biochem. Biophys. Res. Commun. 195:717-722(1993).			
RN	[6]			

SEQUENCE OF 28-193, AND DISULFIDE BONDS.
TISSUE-Urine;
MEDLINE=86140080; PubMed=3949763;
Lai P.H., Everett R., Wang F.F., Arakawa T., Goldwasser E.;
RT "Structural characterization of human erythropoietin.";
J. Biol. Chem. 261:3116-3121(1986).
[7]
RP PRELIMINARY SEQUENCE OF 28-57.
RX MEDLINE=84135751; PubMed=6696989;
RA Yanagawa S., Hirade K., Ohnata H., Sasaki R., Chiba H., Ueda M.,
Goto M.;
RT "Isolation of human erythropoietin with monoclonal antibodies.";
J. Biol. Chem. 259:2707-2710(1984).
[8]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=88153657; PubMed=3346214;
RA Takeuchi M., Takasaki S., Miyazaki H., Kato T., Hoshi S., Kochibe N.,
Kobata A.;
RT "Comparative study of the asparagine-linked sugar chains of human
erythropoietins purified from urine and the culture medium of
recombinant Chinese hamster ovary cells.";
J. Biol. Chem. 263:3657-3663(1988).
[9]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=89118279; PubMed=3219367;
RA Sasaki H., Ochi N., Dell A., Fukuda M.;
RT "Site-specific glycosylation of human recombinant erythropoietin:
analysis of glycopeptides or peptides at each glycosylation site by
fast atom bombardment mass spectrometry.";
J. Biochem. 27:8618-8626(1988).
[10]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=92314463; PubMed=1820196;
RA Takeuchi M., Kobata A.;
RT "Structures and functional roles of the sugar chains of human
erythropoietins.";
Glycobiology 1:337-346(1991).
[11]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=98445092; PubMed=9774108; DOI=10.1038/26773;
Shed R.S., Reid S.W., Li C., Cheetham J.C., Aoki K.H., Liu B.,
Zhan H., Oselund T.D., Chirino A.J., Zhang J., Finer-Moore J.,
Elliot S., Siney K., Katz B.A., Matthews D.J., Wendoloski J.J.,
Egrie J., Stroud R.M.;
RT "Efficiency of signalling through cytokine receptors depends
critically on receptor orientation.";
Nature 395:511-516(1998).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
regulation of erythrocyte differentiation and the maintenance of a
physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
and by liver of fetal or neonatal mammals.
CC -!- PHARMACOLOGICAL: Used for the treatment of anemia. Available under
the names Epogen (Amgen), Epogin (Chugai), Epomax (Elanex), Eprex
(Janssen-Cilag), Neorecomon or Recormon (Roche), and Procrit
(Ortho Biotech). Variations in the glycosylation pattern of EPO
distinguishes these products. Epogen, Epogin, Eprex and Procrit
are generically known as epoetin alfa, Neorecomon and Recormon as
epoetin beta and Epomax as epoetin omega.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
CC -!- DATABASE: NAME=R&D Systems' cytokine source book: EPO;
WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=197".

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EMBL; X02158; CAA26095.1; -.

DR EMBL; X02157; CAA26094.1; -.
DR EMBL; M11319; AAA52400.1; -.
DR EMBL; AF053356; AAC78791.1; -.
DR EMBL; AF203308; AAF23132.1; -.
DR EMBL; AF203306; AAF23132.1; JOINED.
DR EMBL; AF203307; AAF23132.1; JOINED.
DR EMBL; AF203310; AAF23133.1; -.
DR EMBL; AF203309; AAF23133.1; JOINED.
DR EMBL; AF203311; AAF17572.1; -.
DR EMBL; AF203314; AAF23134.1; -.
DR EMBL; AF203312; AAF23134.1; JOINED.
DR EMBL; AF203313; AAF23134.1; JOINED.
DR EMBL; S65458; AAD13964.1; -.
DR PIR; A01855; ZUHU.
DR PDB; 1BUY; NMR; A=28-193.
DR PDB; 1CN4; X-ray; C=28-193.
DR PDB; 1EER; X-ray; A=28-193.
DR GlycoSuiteDB; P01588; -.
DR Genew; HGNC:3415; EPO.
DR MIM; 133170; -.
DR GO; GO:0005615; Extracellular space; TAS.
DR GO; GO:0006950; Response to stress; TAS.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003123; EPO TPO.
DR InterPro; IPR003013; Erythroptn.
DR Pfam; PF00758; EPO TPO; 1.
DR PIRSF; PIRSF001951; EPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO TPO; 1.
DR 3D-structure; Direct protein sequencing; Erythrocyte maturation;
KW Glycoprotein; Hormone; Pharmaceutical; Polymorphism; Signal.
FT SIGNAL 1 27 Erythropoietin.
FT CHAIN 28 193 Removed in mature form (Probable).
FT PROPEP 190 193
FT DISULFID 34 188
FT DISULFID 56 60
FT CARBOHYD 51 51 N-linked (GLCNAC. . .).
FT FTID-CAR 000052. /FTID=CAR 000052.
FT CARBOHYD 65 65 N-linked (GLCNAC. . .).
FT CARBOHYD 110 110 /FTID-CAR 000166. /FTID=CAR 000166.
FT CARBOHYD 153 153 N-linked (GLCNAC. . .).
FT VARIANT 131 132 O-linked (GALNAC. . .).
FT SL -> NF (in an hepatocellular carcinoma).
FT /FTID=VAR 009870. /FTID=VAR 009870.
FT P -> Q (in an hepatocellular carcinoma).
FT /FTID=VAR 009871. /FTID=VAR 009871.
FT CONFLICT 40 40 E -> Q (in Ref. 1; CAA26095).
FT CONFLICT 85 85 Q -> Q (in Ref. 5).
FT CONFLICT 140 140 G -> R (in Ref. 1; CAA26095).
FT HELIX 32 34
FT HELIX 36 52
FT HELIX 53 55
FT TURN 57 58
FT STRAND 61 68
FT STRAND 73 73
FT HELIX 75 78
FT TURN 79 80
FT HELIX 83 109
FT HELIX 118 138
FT TURN 139 140
FT HELIX 141 147
FT TURN 148 149
FT STRAND 160 164
FT HELIX 165 177
FT TURN 178 178
FT HELIX 179 188
SQ SEQUENCE 193 AA; 21306 MW; C91F0E4C26A52033 CRC64;
Query Match 94.8%; Score 851; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	9	APPLRICDSRVLYRLLYLEAKSAENITTCGAHCSLNENITVPDTKVNFYAKRMVEVGOQA	68
Db	28	APPLRICDSRVLYRLLYLEAKSAENITTCGAHCSLNENITVPDTKVNFYAKRMVEVGOQA	87
Qy	69	VEVWQGLALSEAIVLRQALLVNSSQWPEPLQHVDKAVSGLRSLTTLRALGAQKEATS	128
Db	88	VEVWQGLALSEAIVLRQALLVNSSQWPEPLQHVDKAVSGLRSLTTLRALGAQKEATS	147
Qy	129	PPDAASAAPLTIITADTFPKLFRVYSNFIIRGKLIKLYTGEACTGDR	174
Db	148	PPDAASAAPLTIITADTFPKLFRVYSNFIIRGKLIKLYTGEACTGDR	193

```

RESULT 2
AAP22357
ID      AAP22357      PRELIMINARY;      PRT;      193 AA.
AC      AAP22357;
DT      02-MAR-2004      (TrEMBLrel. 27, Created)
DT      02-MAR-2004      (TrEMBLrel. 27, Last sequence update)
DT      02-MAR-2004      (TrEMBLrel. 27, Last annotation update)
DE      Hypothetical protein EPO.
GN      EPO.
OS      Homo sapiens (Human) .
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99063792; PubMed=9847074;
RA      Wilson R.;
RT      "Toward a complete human genome sequence.";
RL      Genome Res. 8:1097-1108(1998) .
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Doebber A., Elliott G., Jones T., Nguyen C., Stoneking T., Sun H.;
RT      "The sequence of Homo sapiens BAC clone RP11-336D7.";
RL      Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

```

RN	[3]
RP	SEQUENCE FROM N.A.
RA	Waterston R.H.;
RL	Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN	[4]
RP	SEQUENCE FROM N.A.
RA	Waterston R.I;
RL	Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RN	[5]
RP	SEQUENCE FROM N.A.
RA	Waterston R.;
RL	Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AC009488; AAP22357.1; --
KW	Hypothetical protein.
SQ	SEQUENCE 193 AA; 21307 MW; C91F0E4C26A52033 CRC64;
 Query Match 94.8%; Score 851; DB 2; Length 193; Best Local Similarity 100.0% Matches 166; Conservative 0; Pred. No. 2.3e-71; Indels 0; Mismatches 0; Indels 0; Gaps 0;	

Qy	9	APPLRICDSRVLYRLYLEAKEAENITTCGAEHCSLNENITVPD	68
Db	28	APPLRICDSRVLYRLYLEAKEAENITTCGAEHCSLNENITVPD	87
Qy	69	VEVQGLALISEAVLRGQALLVNSSQPWEPQLQHVDKAVSG	128
Db	88	VEVQGLALISEAVLRGQALLVNSSQPWEPQLQHVDKAVSG	147
Qy	129	PPDAASAAPRTITADTFRKLFVYNSFLRGKLYTGCACTGDR	174
Db	148	PPDAASAAPRTITADTFRKLFVYNSFLRGKLYTGCACTGDR	193

RESULT 3
EPO MACFA

ID	EPO_MACFA	STANDARD;	PRT;	192 AA.
AC	P07865;			
DT	01-AUG-1988	(Rel. 08, Created)		
DT	01-AUG-1988	(Rel. 08, Last sequence update)		
DT	05-JUL-2004	(Rel. 44, Last annotation update)		
DE	Erythropoietin precursor.			
GN	Name=EPO;			
OS	Macaca fascicularis	(Crab eating macaque) (Cynomolgus monkey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;			
OC	Cercopithecinae; Macaca.			
OX	NCBI_TaxID=9541;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87055236;	PubMed=2877922;		
RA	Lin F.-K., Lin C.-H., Lai P.-H., Browne J.K., Egrie J.C., Smalling R.,			
RA	Fox G.M., Chen K.K., Castro M., Suggs S.;			
RT	"Monkey erythropoietin gene: cloning, expression and comparison with			
RT	the human erythropoietin gene.";			
RL	Gene 44:201-209(1986).			
CC	-!- FUNCTION:	Erythropoietin is the principal hormone involved in the regulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.		
CC	-!- SUBCELLULAR LOCATION:	Circulated.		
CC	-!- TISSUE SPECIFICITY:	Produced by kidney or liver of adult mammals and by liver of fetal or neonatal mammals.		
CC	-!- SIMILARITY:	Belongs to the EPO / TPO family.		
CC	-----			
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CC	-----			
DR	EMBL;	M18189; AAA36841.1;	--	
DR	PIR;	JQ0173; JQ0173.		
DR	HSPG;	P01588; ICN4.		
DR	InterPro;	IPR009079; 4_helix_cytokine.		
DR	InterPro;	IPR001323; EPO.TPO.		
DR	InterPro;	IPR003013; Erythroptn.		
DR	Pfam;	PF00758; EPO.TPO; 1.		
DR	PfRSF;	PFRS001951; EPO; 1.		
DR	PRINTS;	PR0272; ERYTHROPTN.		
DR	PROSITE;	PS00817; EPO.TPO; 1.		
KW	Erythrocyte maturation; Glycoprotein; Hormone; Signal.			
FT	SIGNAL	1 27	By similarity.	
FT	CHAIN	28 192	Erythropoietin.	
FT	DISULFID	34 187	By similarity.	
FT	DISULFID	56 60	By similarity.	
FT	CARBOHYD	51 51	N-linked (GLCNAC...) (By similarity).	
FT	CARBOHYD	55 65	N-linked (GLCNAC...) (By similarity).	
FT	CARBOHYD	110 110	N-linked (GLCNAC...) (By similarity).	
FT	CARBOHYD	152 152	O-linked (GalNAc...) (By similarity).	
SEQ	SEQUENCE	192 AA; 21113 MW; B8A900F442AD4522 CRC64;		
Query Match		85.8%;	Score 770.5;	DB 1; Length 192;
Best Local Similarity		89.5%;	Pred. No. 7.7e-64;	
Matches 154; Conservative		7; Mismatches 6;	Indels 5; Gaps 2;	
QY	3	PGAHHVAPRLICDSRVLELYLLEAKEAEENITTCGAHCSCSLNENITVPDTKNFYAWKRM	62	
Dd	26	PG----APRLICDSRVLELYLLEAKEAEENVTCGCSCSLNENITVPDTKNFYAWKRM	81	
QY	63	EVGQQAVEVVOGGLALLSEAVLRGQALLVNVSQPWEPLQLHVDKAVSGLSRLTLTLRALGA	122	
Dd	82	EVGQQAVEVVOGGLALLSEAVLRGQAVLANSSQFPPEPLQLHMDKAISGLRSITTLRALGA	141	
QY	123	QKEAISPPDAASAPLRTTTADTKFLFRVSNFLRGKLKYTGECRCGTGR	174	
Dd	142	Q-EAISLPDAASAPLRTTTADTKFLFRVSNFLRGKLKYTGECRCGRD	192	

RESULT 4
EPO_MACMU STANDARD; PRT; 192 AA.
ID EPO_MACMU STANDARD; PRT; 192 AA.
AC Q28513;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Erythropoietin precursor.
GN Name=EPO;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
Czelusniak J., Goodman M., Bunn H.F.;
RA "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -I- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -I- SIMILARITY: Belongs to the EPO / TPO family.
CC
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CC
CC EMBL; L10609; AAA36842.1; -.
CC PIR; I84613; I84613.
CC HSPSP; P01588; 1CN4.
CC InterPro; IPR009079; 4 helix_cytokine.
CC InterPro; IPR001323; EPO_TPO.
CC InterPro; IPR003013; Erythroptn.
CC Pfam; PF00758; EPO_TPO; 1.
CC PIRSF; PIRSF001951; EPO; 1.
CC PRINTS; PR00272; ERYTHROPTN.
CC PROSITE; PS00817; EPO_TPO; 1.
CC Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 27
FT CHAIN 1 27
FT DISULFID 34 187
FT DISULFID 56 60
FT DISULFID 51 51 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 51 51 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 65 65 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 110 110 O-linked (GlcNAc...) (By similarity).
FT CARBOHYD 152 152
SQ SEQUENCE 192 AA; 21081 MW; 275560A264628CD1 CRC64;
Query Match 85.2%; Score 765.5; DB 1; Length 192;
Best Local Similarity 88.4%; Pred. No. 2.3e-63;
Matches 152; Conservative 9; Mismatches 6; Indels 5; Gaps 2;
QY 3 PGAAHYAPPRICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVNFKYAKRM 62
DB 26 PG-----APPRLVCDSSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVNFKYAKRI 81
QY 63 EVGQQAWEVWQGLALLSAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGA 122
DB 82 EVGQQAWEVWQGLALLSAVLRGQAVLANSQPWEPLQLHMDKAVSGLSRLTLLRALGA 141

QY 123 QKEAISPPDAASAPLRTITADTFKRLFRVSNFLRGLKLYTGEACRTGDR 174
DB 142 Q-EAISLPDAASAPLRTITADTFCKLFRVSNFLRGLKLYTGEACRRGDR 192
RESULT 5
Q867B1 PRELIMINARY; PRT; 192 AA.
ID Q867B1;
AC Q867B1;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Erythropoietin.
GN Name=EPO;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=14719696;
RA Sato F., Yamashita S., Kugo T., Hasegawa T., Mitsui I.,
RA Kijima-Suda I.;
RA "Nucleotide sequence of equine erythropoietin and characterization of
RT region-specific antibodies.";
RL Am. J. Vet. Res. 65:15-19(2004).
DR EMBL; AB100030; BAC55239.1; -.
DR HSPSP; P01588; 1BUV.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR009079; 4 helix_cytokine.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PIRSF; PIRSF001951; EPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
SQ SEQUENCE 192 AA; 20984 MW; E02D09849B09C4F CRC64;
Query Match 81.1%; Score 728; DB 2; Length 192;
Best Local Similarity 84.9%; Pred. No. 7.3e-60;
Matches 141; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
QY 9 APRRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVNFKYAKRMVEVQQA 68
DB 27 APRRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVNFKYAKRMVEVQQA 86
QY 69 VEVWQGLALLSAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 128
DB 87 VEVWQGLALLSAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 146
QY 129 PDAASAPLRTITADTFKRLFRVSNFLRGLKLYTGEACRTGDR 174
DB 147 PDAASAPLRTITADTFCKLFRVSNFLRGLKLYTGEACRRGDR 192
RESULT 6
EPO_FELCA STANDARD; PRT; 192 AA.
ID EPO_FELCA
AC P33708;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Erythropoietin precursor.
GN Name=EPO;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.

Matches 139; Conservative 8; Mismatches 19; Indels 1; Gaps 1;

Qy 9 APPRLICDSRVLYLEAEAEENITTCGAHCSLNENITVPTKKNFYAKRMEVQQA 68
 Db 26 APARLICDSRVLYLEAEAEENITTCGAHCSLNENITVPTKKNFYAKRMEVQQA 85
 Qy 69 VEVWQGLALLSEAVLRQALLVNSQWPELQHLVDKAVSGLSLTLLRALGAQKEAIS 128
 Db 86 LEVWQGLALLSEAILRQALLANASQCEALRLHVDKAVSGLSLTLLRALGAQKEAIS 145
 Qy 129 PPDAA-SAAPLRTITADTFKLFVYSNFLRGKLYTGACRTGDR 174
 Db 146 LPDAPSAAPLRAFTVDALSKLFVYSNFLRGKLYTGACRRGDR 192

RESULT 11
 EPO_MOUSE
 ID EPO_MOUSE STANDARD; PRT; 192 AA.
 AC P07321;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=Epo;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87039105; PubMed=3773894;
 RA Shoemaker C.B., Mitsock L.D.;
 RT "Murine erythropoietin gene: cloning, expression, and human gene
 RT homology.";
 RL Mol. Cell. Biol. 6:849-858 (1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87039104; PubMed=3022133;
 RA McDonald J.D., Lin F.-K., Goldwasser E.;
 RT "Cloning, sequencing, and evolutionary analysis of the mouse
 RT erythropoietin gene.";
 RL Mol. Cell. Biol. 6:842-848 (1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RX MEDLINE=21138439; PubMed=11239002;
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
 RA Miller W., Koop B.F.;
 RT "Comparative analysis of the gene-dense ACHE/TFR2 region on human
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";
 RL Nucleic Acids Res. 29:1352-1365 (2001).
 RN [4]
 RP SEQUENCE OF 1-52 FROM N.A.
 RC STRAIN=ICFW;
 RX MEDLINE=98030528; PubMed=9365246;
 RA Chretien S., Duprez V., Maoche L., Gisselbrecht S., Mayeux P.,
 RA Lacombe C.;
 RT "Abnormal erythropoietin (Epo) gene expression in the murine
 RT erythroleukemia IM32 cells results from a rearrangement between the G-
 RT protein beta2 subunit gene and the Epo gene.";
 RL Oncogene 15:1995-1999 (1997).
 CC -1- FUNCTION: Erythropoietin is the principal hormone involved in the
 CC regulation of erythrocyte differentiation and the maintenance of a
 CC physiological level of circulating erythrocyte mass.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 CC and by liver of fetal or neonatal mammals.
 CC -1- SIMILARITY: Belongs to the EPO / TPO family.
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 CC -----
 DR EMBL; M12482; AAA37568.1; -;
 DR EMBL; M12930; AAA37570.1; -;
 DR EMBL; AF112033; AK28825.1; -;
 DR EMBL; Y11971; CAAT2707.1; -;
 DR PIR; A24902; A24902.
 DR HSSP; P01588; 1CN4.
 DR MGD; MGI:95407; Epo.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR01323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 192 Erythropoietin.
 FT DISULFID 33 187 By similarity.
 FT CARBOHYD 50 50 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 64 64 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 109 109 N-linked (GlcNAc...) (By similarity).
 SQ SEQUENCE 192 AA; 21365 MW; 65F94E214E0DEF2E CRC64;
 Query Match 77.3%; Score 694; DB 1; Length 192;
 Best Local Similarity 80.1%; Pred. No. 1;le-56;
 Matches 133; Conservative 14; Mismatches 19; Indels 0; Gaps 0;
 Qy 9 APPRLICDSRVLYLEAEAEENITTCGAHCSLNENITVPTKKNFYAKRMEVQQA 68
 Db 27 APPRLICDSRVLYLEAEAEENITTCGAHCSLNENITVPTKKNFYAKRMEVQQA 86
 Qy 69 VEVWQGLALLSEAVLRQALLVNSQWPELQHLVDKAVSGLSLTLLRALGAQKEAIS 128
 Db 87 IEVWQGLALLSEAILRQALLANASQCEALRLHVDKAVSGLSLTLLRALGAQKEAIS 146
 Qy 129 PPDAA-SAAPLRTITADTFKLFVYSNFLRGKLYTGACRTGDR 174
 Db 147 PPDTPPAPLRTITVDFCKLFVYSNFLRGKLYTGACRRGDR 192

RESULT 12
 EPO_SHEEP
 ID EPO_SHEEP STANDARD; PRT; 194 AA.
 AC P33709; Q28572;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=Epo;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Ruminantia; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93351736; PubMed=8349021;
 RA Fu P., Evans B., Lim G.B., Moritz K., Wintour M.E.;
 RT "The sheep erythropoietin gene: molecular cloning and effect of
 RT hemorrhage on plasma erythropoietin and renal/liver messenger RNA in
 RT adult sheep.";
 RL Mol. Cell. Endocrinol. 93:107-116 (1993).
 RN [2]
 RP SEQUENCE OF 4-194 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,

RA Czelusniak J., Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 RL sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 CC -1- FUNCTION: Erythropoietin is the principal hormone involved in the
 CC regulation of erythrocyte differentiation and the maintenance of a
 CC physiological level of circulating erythrocyte mass.
 CC SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 CC and by liver of fetal or neonatal mammals.
 CC -1- SIMILARITY: Belongs to the EPO / TPO family.
 CC -----
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 CC -----
 DR EMBL; Z24681; CAA08048.1; -;
 DR EMBL; L10610; AAA31518.1; -;
 DR PIR; I46401; I46401.
 DR HSSP; P01588; 1CN4.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 27 By similarity.
 FT CHAIN 28 194 Erythropoietin.
 FT DISULFID 34 189 By similarity.
 FT DISULFID 56 60 By similarity.
 FT CARBOHYD 51 51 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 65 65 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 16 16 F -> L (in Ref. 2).
 FT CONFLICT 108 108 L -> P (in Ref. 2).
 SQ SEQUENCE 194 AA; 21335 MW; C025AAB0528131A9 CRC64;
 Query Match 76.9%; Score 690.5; DB 1; Length 194;
 Best Local Similarity 82.0%; Pred. No. 2.4e-56;
 Matches 137; Conservative 9; Mismatches 20; Indels 1; Gaps 1;
 QY 9 APPRLICDSRVLEYLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVQQA 68
 Db 28 APPRLICDSRVLEYLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVQQA 87
 QY 69 VEVWQGLALSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
 Db 88 LEVWQGLALSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIP 147
 QY 129 PPDAA-SAAPLRITATDFKLFVYGNFLRGKLYTGACRTGDR 174
 Db 148 LPDATSAAPLRITVDAKSLFRVYGNFLRGKLYTGACRTGDR 194
 Query Match 76.9%; Score 690.5; DB 1; Length 194;
 Best Local Similarity 82.0%; Pred. No. 2.4e-56;
 Matches 137; Conservative 9; Mismatches 20; Indels 1; Gaps 1;
 QY 9 APPRLICDSRVLEYLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVQQA 68
 Db 28 APPRLICDSRVLEYLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVQQA 87
 QY 69 VEVWQGLALSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
 Db 88 LEVWQGLALSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIP 147
 QY 129 PPDAA-SAAPLRITATDFKLFVYGNFLRGKLYTGACRTGDR 174
 Db 148 LPDATSAAPLRITVDAKSLFRVYGNFLRGKLYTGACRTGDR 194
 RESULT 13
 Q9GKA2
 ID Q9GKA2 PRELIMINARY; PRT; 195 AA.
 DT 01-MAR-2001 (TrEMBLrel. 15, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Erythropoietin.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 ON NCBI_TaxID=9986;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21290682; PubMed=11396976;
 RA Vilalta A., Wu D., Margalith M., Hobart P.;
 RT "Rabbit EPO gene and cDNA: expression of rabbit EPO after
 RL intramuscular injection of pDNA.";
 RL Biochem. Biophys. Res. Commun. 284:823-827(2001).
 DR EMBL; AF290944; AAG36962.1; -;
 DR HSSP; P01588; 1CN4.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 SQ SEQUENCE 195 AA; 21025 MW; 1F1DC7F403A303BC CRC64;
 Query Match 76.3%; Score 685.5; DB 2; Length 195;
 Best Local Similarity 81.4%; Pred. No. 7e-56;
 Matches 136; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
 QY 9 APPRLICDSRVLEYLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVQQA 68
 Db 29 APPRLICDSRVLEYLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKMEVQQA 88
 QY 69 VEVWQGLALSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 128
 Db 89 VEVWQGLALSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 148
 QY 129 PPDAA-SAAPLRITATDFKLFVYGNFLRGKLYTGACRTGDR 174
 Db 149 PPEAASAAPLRTVAADTLCKLFYVYGNFLRGKLYTGACRTGDR 195
 RESULT 14
 Q9GKA3
 ID Q9GKA3 PRELIMINARY; PRT; 195 AA.
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Erythropoietin.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 ON NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21290682; PubMed=11396976;
 RA Vilalta A., Wu D., Margalith M., Hobart P.;
 RT "Rabbit EPO gene and cDNA: expression of rabbit EPO after
 RL intramuscular injection of pDNA.";
 RL Biochem. Biophys. Res. Commun. 284:823-827(2001).
 DR EMBL; AF290943; AAG36961.1; -;
 DR PIR; JC7699; JC7699.
 DR HSSP; P01588; 1CN4.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 SQ SEQUENCE 195 AA; 21053 MW; 0999DA7D852713F3 CRC64;
 Query Match 76.3%; Score 685.5; DB 2; Length 195;
 Best Local Similarity 81.4%; Pred. No. 7e-56;
 Matches 136; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

Matches 136; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
Query Match 76.1%; Score 683; DB 1; Length 190;
Best Local Similarity 82.1%; Pred. No. 1.2e-55;
Matches 138; Conservative 7; Mismatches 21; Indels 2; Gaps 1;
QY 9 APPRLICDSRVLELYLLEAKEAENITTCGAHCSCSLNENITVPDTKVNFYAKRMEVGOQA 68
DB 29 APARLICDSRVLELYLLEAKEAENITTCGAHCSCSLNENITVPDTKVNFHHKKSEAGRA 88
QY 69 VEWQGLALLSEAVLRGQALLVNSQWPEFLQHVVDKAVSGRLSTLLRALGAQKEAIS 128
DB 89 VEWQGLALLSEAVLRGQALLVNSQWPEFLQHVVDKAVSGRLSTLLRALGVQKEAVS 148
QY 129 PPDA--SAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 174
DB 149 PPEAASSAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGDR 195

Search completed: November 19, 2004, 21:11:00
Job time : 104.996 secs

RESULT 15

EPO_PIG STANDARD; PRT; 190 AA.
AC P49157;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Erythropoietin precursor (Fragment).
GN Name=EPO;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
RA Czelusniak J., Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
sequence homology among mammals";
RL Blood 82:1507-1516(1993).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
regulation of erythrocyte differentiation and the maintenance of a
physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.

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EMBL; LI0607; AAA31029.1; -
PIR; I46578; I46578.
DR HSSP; P01588; 1CN4.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR001323; EPO_TPO_
DR InterPro; IPR003013; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT NON_TER 1
FT SIGNAL <1 22 Potential
FT CHAIN 23 190 Erythropoietin.
FT DISULFID 29 185 By similarity.
FT DISULFID 51 55 By similarity.
FT CARBOHYD 46 46 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 60 60 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 105 105 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 168 168 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 190 AA; 20888 MW; A75BD6CCES077E2A CRC64;

